



# **STIC Search Report**

## **Biotech-Chem Library**

**STIC Database Tracking Number: 141622**

**TO: Bennett Celsa**  
**Location: rem/2a25/2a05**  
**Art Unit: 1639**  
**Thursday, January 06, 2005**

**Case Serial Number: 09/748739**

**From: Alex Waclawiw**  
**Location: Biotech-Chem Library**  
**Rem 1A71**  
**Phone: 272-2534**

**Alexandra.waclawiw@uspto.gov**

### **Search Notes**

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Need  
by

1/12/05

Access DB# 141622

## SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: BENNETT CELSA Examiner #: 73815 Date: 1/13/05  
Art Unit: 1639 Phone Number: 202-272-0807 Serial Number: 0991748739  
Mail Box and Bldg/Room Location: 571 Results Format Preferred (circle): PAPER DISK 5-MAIL

2A05 → REMSEN 2A35 2A25

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: BUTYRCHOLINE esterase variants } see attached  
Inventors (please provide full names): LOCKRIDGE WATKINS } B2B

Earliest Priority Filing Date: 12/26/00

\*For Sequence Searches Only\* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please  
IN RELEVANT DATABASES: (see claim 1)

1. SEQ SEARCH of:

≥ 95% Identity to 1-602 of seq 2  
AND aa-602 m.

≥ 95% Identity to 29-602 of seq 2

NOTE FYI: TRP must be present AT  
Position 356 (NOT 328) of seq 2

2. PERCEKON INTERFERENCE search  
for above

Attached  
1. B2B  
2. Claims 192

Point of Contact:  
Alexandra Wacławiw  
Technical Info. Specialist  
GMT 0A02 Tel: 308-4491  
P.U. 1-6-05  
S.D. 1-6-05

thanks

EX CELSA - 20807

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 6, 2005, 09:27:17 ; Search time 197 seconds  
(without alignments)  
1758.251 Million cell updates/sec

Title: US-09-748-739A-2

Perfect score: 3260  
Sequence: 1 MDSKVITICIRFLFWPLLCL.....MDMKQFNVDYTSKKSCVGL 602

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : UniProt\_02:.\*  
1: uniprot\_sprot:.\*  
2: uniprot\_trembl:.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3239	99.4	602	1	CHLE_HUMAN
2	2858	87.7	602	1	Q9NIN9
3	2855.5	87.6	581	1	CHLE_RABIT
4	2784	85.4	602	1	CHLE_FELCA
5	2774	85.1	574	1	CHLE_HORSE
6	2772	85.0	602	1	CHLE_PANTT
7	2602	79.8	603	2	BAC34196
8	2593	79.5	603	1	CHLE_MOUSE
9	2588	79.4	597	2	Q9JKE1
10	2339.5	71.8	603	2	Q90ZK8
11	1777	54.5	633	1	ACES_ELEBL
12	1766.5	54.2	634	1	ACES_BRABE
13	1730.5	53.1	606	1	ACES_BUNFA
14	1698.5	52.1	614	1	ACES_HUMAN
15	1698.5	52.1	614	2	AP23465
16	1693.5	51.9	614	1	ACES_RAT
17	1692.5	51.9	614	1	ACES_MOUSE
18	1692.5	51.9	614	2	BAC31228
19	1692.5	51.9	614	2	BAC31641
20	1692.5	51.9	614	2	BAC32595
21	1683	51.6	611	1	ACES_FELCA
22	1674	51.3	349	2	Q9GKT6
23	1674	51.3	613	1	ACES_BOVIN
24	1654	50.7	586	1	ACES_TORCA
25	1649.5	50.6	590	1	ACES_TORCA
26	1649.5	50.6	584	1	ACES_RABIT
27	1567	48.1	767	2	Q86TM9
28	1466	45.0	617	2	ACES_CHICK
29	1449	44.4	602	2	Q76959
30	1390	42.6	605	2	Q76998
31	1367.5	41.9	526	2	Q86YX9

32	1324	40.6	701	2	Q75VX9	Q75VX9 culcx trita
33	1324	40.6	701	2	BAD06210	BAD06210 culcx trit
34	1317	40.4	702	1	ACES_CULPI	Q86GC8 culcx pipie
35	1303	40.0	623	2	Q7RTM0	Q7RTM0 anophelies g
36	1303	40.0	737	1	ACE1_ANOGA	Q869C3 anophelies g
37	1303	40.0	743	2	Q7PUN2	Q7PUN2 anophelies g
38	1295	39.7	559	2	Q7PKM1	Q7PKM1 anophelies g
39	1279	39.2	687	2	Q86CZ4	Q86CZ4 tetranychus
40	1222.5	37.5	676	2	Q9BMJ1	Q9BMJ1 schizaphis
41	1218.5	37.4	660	2	Q6KAV3	Q6KAV3 aphis gossy
42	1215.5	37.3	671	2	Q6KAV4	Q6KAV4 aphis gossy
43	1214.5	37.3	676	2	Q8MV35	Q8MV35 aphis gossy
44	1211.5	37.2	676	2	Q6KAV5	Q6KAV5 aphis gossy
45	1206	37.0	610	2	Q9J110	Q9J110 loligo opal
46	1177.5	36.1	677	2	Q9NMJ6	Q9NMJ6 nephotetrix
47	1172	36.0	656	2	Q96529	Q96529 meloidogyne
48	1166	35.8	656	2	Q9XVX9	Q9XVX9 meloidogyne
49	1153	35.4	620	1	ACE1_CABBR	Q27459 caenorhabdi
50	1152	35.3	638	2	Q86QW5	Q86QW5 heliocoverpa
51	1149	35.2	647	2	Q8MX85	Q8MX85 heliocoverpa
52	1142	35.0	620	1	ACES_LEPDE	P38433 caenorhabdi
53	1140.5	35.0	629	1	ACES_LEPDE	Q27677 leptonotars
54	1134	34.8	638	2	Q8MZL2	Q8MZL2 pluteella xy
55	1127	34.6	585	2	Q7RTL6	Q7RTL6 ciona intes
56	1088.5	33.4	550	2	Q7RTL7	Q7RTL7 ciona savig
57	1079	33.1	587	2	Q6XR74	Q6XR74 rhinicephal
58	1079	33.1	587	2	AP49302	AP49302 rhinicephal
59	1079	33.1	593	2	Q6XR75	Q6XR75 rhinicephal
60	1079	33.1	593	2	AP49301	AP49301 rhinicephal
61	1075.5	33.0	637	2	Q9TX11	Q9TX11 aedes aegypt
62	1074.5	33.0	590	2	Q61987	Q61987 boophilus d
63	1069.5	32.8	596	2	Q6XR73	Q6XR73 dermacentor
64	1069.5	32.8	545	2	AP49303	AP49303 dermacent
65	1063.5	32.6	645	2	Q7OR60	Q7OR60 anophelies g
66	1063.5	32.6	645	2	Q7RTI9	Q7RTI9 anophelies g
67	1059.5	32.5	664	1	ACES_ANOST	Q75VY0 anophelies g
68	1055.5	32.4	633	2	Q75VY0	Q75VY0 culcx trita
69	1055.5	32.4	633	2	BAD06209	BAD06209 culcx trit
70	1050	32.2	692	2	Q95P20	Q95P20 musca domes
71	1050	32.2	692	2	Q95W7	Q95W7 musca domes
72	1048	32.1	692	2	Q8MXC6	Q8MXC6 musca domes
73	1048	32.1	692	2	Q8MXC8	Q8MXC8 musca domes
74	1048	32.1	692	2	Q8MXC9	Q8MXC9 musca domes
75	1047.5	32.1	595	2	Q45210	Q45210 boophilus m
76	1045	32.0	692	2	Q8MXC4	Q8MXC4 musca domes
77	1044	32.0	649	1	ACES_DROME	P07140 dtrosophila
78	1042.5	32.0	510	2	Q7YZE7	Q7YZE7 trialeurode
79	1042	32.0	691	2	Q8MXC5	Q8MXC5 musca domes
80	1041.5	31.9	664	2	Q8T7U9	Q8T7U9 myzus persi
81	1041	31.9	692	2	Q8MXC7	Q8MXC7 musca domes
82	1038.5	31.9	612	2	Q8MU94	Q8MU94 musca domes
83	1033.5	31.7	604	1	ACE4_CABBR	Q9NDG8 caenorhabdi
84	1033	31.7	692	2	Q7YWC9	Q7YWC9 musca domes
85	1029.5	31.6	708	2	P91954	P91954 lucilia cup
86	1029	31.6	673	2	Q8MWZ4	Q8MWZ4 bactrocera
87	1028.5	31.5	603	2	Q7YZO0	Q7YZO0 myzus persi
88	1025.5	31.5	602	2	Q61372	Q61372 caenorhabdi
89	1025	31.5	528	2	Q62563	Q62563 tripticephal
90	1014.5	31.1	338	1	ACES_MYXGL	Q92081 myxine glut
91	1014.5	31.1	461	2	Q8MV36	Q8MV36 aphis gossy
92	1008	30.9	461	2	Q7YZP8	Q7YZP8 bemisia tab
93	963.5	29.6	615	2	Q86GJ7	Q86GJ7 dictyocaulu
94	963	29.5	492	2	Q9GDP7	Q9GDP7 aphs mellif
95	959	29.4	512	2	Q8MZM0	Q8MZM0 pluteella xy
96	957.5	29.4	629	2	Q61378	Q61378 caenorhabdi
97	951	29.2	594	2	Q81786	Q81786 necator ame
98	951	29.2	629	2	Q61371	Q61371 caenorhabdi
99	950.5	29.2	613	2	Q6XPY6	Q6XPY6 dictyocaulu
100	950.5	29.2	613	2	AA062949	AA062949 dictyocaulu

## ALIGNMENTS

RESULT 1  
 CHIE\_HUMAN STANDARD; PRT; 602 AA.  
 ID CHIE\_HUMAN  
 AC P06276;  
 DT 01-JAN-1988 (Rel. 06, Created)  
 DT 01-AUG-1988 (Rel. 08, Last sequence update)  
 DT 01-OCT-2004 (Rel. 45, Last annotation update)  
 DE Cholinesterase precursor (EC 3.1.1.8) (Acylcholine acylhydrolase)  
 DE (Choline esterase II) (Butyrylcholine esterase)  
 DE (Pseudochoolinesterase).  
 GN Name=CHBE; Synonyms=CHB1;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90212557; PubMed=2322535;  
 RA Appagou M., Kott M., Vatsis K.F., Bartels C.F., la Du B.N.,  
 RA Lockridge O.,  
 RT "Structure of the gene for human butyrylcholinesterase. Evidence for a  
 RT single copy.";  
 RL Biochemistry 29:124-131(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87231856; PubMed=3035536;  
 RA Prody C.A., Zevin-Sonkin D., Ghatt A., Goldberg O., Soreq H.,  
 RT "Isolation and characterization of full-length cDNA clones coding for  
 RT cholinesterase from fetal human tissues.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 84:3555-3559(1987).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88016155; PubMed=3477799;  
 RA McIernan C., Adkins S., Chaconnet A., Vaughan T.A., Bartels C.F.,  
 RA Kott M., Rosenberry T.L., la Du B.N., Lockridge O.,  
 RT "Brain cDNA clone for human cholinesterase.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 84:6682-6686(1987).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenman C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stadelton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Rata S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Hellon B., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.N.,  
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.B.,  
 RA Schermer A., Schein J.E., Jones S.J.M., Matra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [5]  
 RP SEQUENCE OF 29-602.  
 RX MEDLINE=87109144; PubMed=3542989;  
 RA Lockridge O., Bartels C.F., Vaughan T.A., Wong C.K., Norton S.E.,  
 RA Johnson L.L.,  
 RT "Complete amino acid sequence of human serum cholinesterase.";  
 RL J. Biol. Chem. 262:549-557(1987).  
 RN [6]

RP DISULFIDE BONDS.  
 RX MEDLINE=88007487; PubMed=3115973;  
 RA Lockridge O., Adkins S., la Du B.N.,  
 RT "Location of disulfide bonds within the sequence of human serum  
 RT cholinesterase.";  
 RL J. Biol. Chem. 262:12945-12952(1987).  
 RN [7]  
 RP REVIEW.  
 RX MEDLINE=89149758; PubMed=3067729;  
 RA Lockridge O.,  
 RT "Structure of human serum cholinesterase.";  
 RL Bioessays 9:125-128(1988).  
 RN [8]  
 RP VARIANT ATYPICAL GUY-98.  
 RX MEDLINE=89128896; PubMed=2915989;  
 RA McGuire M.C., Nogueira C.P., Bartels C.F., Lightstone H., Hajra A.,  
 RA van der Spek A.F.L., Lockridge O., la Du B.N.,  
 RT "Identification of the structural mutation responsible for the  
 RT dibucaine-resistant (atypical) variant form of human serum  
 RT cholinesterase.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 86:953-957(1989).  
 RN [9]  
 RP VARIANT ILB-358.  
 RX MEDLINE=96287386; PubMed=8680411;  
 RA Iida S., Kinoshita M., Fujii H., Moriyama Y., Nakamura Y., Yura N.,  
 RA Moriwaiki K.,  
 RT "Mutations of human butyrylcholinesterase gene in a family with  
 RT hypocholinesterasemia.";  
 RL Hum. Mutat. 6:349-351(1995).  
 CC -1- CATALYTIC ACTIVITY: An acylcholine + H(2)O = choline + a  
 CC carboxylic acid anion.  
 CC -1- SUBUNIT: Homotetramer. The tetramer is composed of two dimers. The  
 CC two subunits in a dimer are linked by a disulfide bond.  
 CC -1- TISSUE SPECIFICITY: Present in most cells except erythrocytes.  
 CC -1- DISEASE: Mutant alleles of CHB1 are responsible for  
 CC hypocholinesterasemia resulting in suxamethonium sensitivity.  
 CC Homozygous persons sustain prolonged apnea after administration of  
 CC the muscle relaxant suxamethonium in connection with surgical  
 CC anesthesia.  
 CC -1- MISCELLANEOUS: Cholinesterase is highly reactive with  
 CC organophosphate esters.  
 CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; M32391; AAA99296.1; -;  
 DR EMBL; M32389; AAA99296.1; JOINED.  
 DR EMBL; M32390; AAA99296.1; JOINED.  
 DR EMBL; M15541; AAA98113.1; -;  
 DR EMBL; M16474; AAA52015.1; -;  
 DR EMBL; BC018141; AAH18141.1; -;  
 DR PIR; A33769; ACNU.  
 DR PDB; 1EHO; Model; A=30-560.  
 DR PDB; 1EHQ; Model; A=30-560.  
 DR PDB; 1P01; X-ray; A=29-557.  
 DR PDB; 1P0P; X-ray; A=29-557.  
 DR PDB; 1P0P; X-ray; A=29-557.  
 DR PDB; 1P0Q; X-ray; A=29-557.  
 DR Genew; HGNC:983; BCHE.  
 DR MIM; 177400; -;  
 DR GO; GO:0001540; F:beta-amyloid binding; NAS.  
 DR GO; GO:0003824; F:catalytic activity; NAS.  
 DR GO; GO:0004104; F:cholinesterase activity; NAS.  
 DR GO; GO:0019899; F:enzyme binding; NAS.  
 DR GO; GO:0050783; P:cocaine metabolism; TAS.  
 DR InterPro; IPR002018; CarboxesteraseB.  
 DR InterPro; IPR000997; Cholinesterase.

DR InterPro; IPR000379; Ser\_estr.  
 DR Pfam; PF00135; Coesterase; 1.  
 DR PRINTS; PR00878; CHOLINESTRASE.  
 DR PROSITE; PS00122; CARBOXYLESTERASE\_B\_1; 1.  
 DR PROSITE; PS00941; CARBOXYLESTERASE\_B\_2; 1.  
 DR 3D-structure; Direct protein sequencing; Disease mutation;  
 KW Glycoprotein; Hydrolase; Polymorphism; Serine esterase; Signal.  
 FT SIGNAL 1 28  
 FT CHAIN 29 602  
 FT ACT\_SITE 226 226 Acyl-ester intermediate (By similarity).  
 FT ACT\_SITE 353 353 Charge relay system (By similarity).  
 FT ACT\_SITE 466 466 Charge relay system (By similarity).  
 FT DISULFID 93 120  
 FT DISULFID 280 291  
 FT DISULFID 428 547  
 FT DISULFID 599 599  
 FT CARBOHYD 45 45 Interchain.  
 FT CARBOHYD 85 85 N-linked (GlcNAc...)  
 FT CARBOHYD 134 134 N-linked (GlcNAc...)  
 FT CARBOHYD 269 269 N-linked (GlcNAc...)  
 FT CARBOHYD 284 284 N-linked (GlcNAc...)  
 FT CARBOHYD 369 369 N-linked (GlcNAc...)  
 FT CARBOHYD 483 483 N-linked (GlcNAc...)  
 FT CARBOHYD 509 509 N-linked (GlcNAc...)  
 FT CARBOHYD 514 514 N-linked (GlcNAc...)  
 FT VARIANT 98 98 D -> G (in atypical form, dibucaine-resistant; dbSNP:1799807).  
 FT VARIANT 271 271 T -> M (in fluoride-1).  
 FT VARIANT 358 358 /FTRD=VAR\_002361.  
 FT VARIANT 418 418 L -> I (in hypocholinerastemia).  
 FT VARIANT 418 418 /FTRD=VAR\_002362.  
 FT VARIANT 567 567 G -> V (in fluoride-2).  
 FT VARIANT 567 567 /FTRD=VAR\_002363.  
 FT VARIANT 567 567 A -> T (in K variant; with reduced enzyme activity; dbSNP:1803274).  
 FT VARIANT 567 567 /FTRD=VAR\_002364.  
 FT SEQUENCE 602 AA; 68418 MW; C9836405D9057F27 CRC64;  
 Query Match 99.4%; Score 3239; DB 1; Length 602;  
 Best Local Similarity 99.7%; Pred. No. 3,1e-23; Matches 600; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

DR 421 VGDYNPICPALFTKKESEWGNNAFFYYFEHRSSKLPWPEWGMVHGYEIEFVGLPLER 480  
 QY 481 RDNYTKAEIILSRIVKRWANPAKYGNPNETONNSTSWPVFKSTEOXYTLTANESTRIMT 540  
 DB 481 RDNYTKAEIILSRIVKRWANPAKYGNPNETONNSTSWPVFKSTEOXYTLTANESTRIMT 540  
 QY 541 KLRAGQCRPMTSFPKYLEMTGNIDEAEWEWKAQFHRMNNYMDWKNQFNDYTSKESCV 600  
 DB 541 KLRAGQCRPMTSFPKYLEMTGNIDEAEWEWKAQFHRMNNYMDWKNQFNDYTSKESCV 600  
 QY 601 GL 602  
 DB 601 GL 602  
 DB 601 GL 602  
 RESULT 2  
 Q9NIN9 PRELIMINARY; PRT; 602 AA.  
 AC Q9NIN9  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DE Butyrylcholinesterase (EC 3.1.1.8).  
 GN Name=BChE;  
 OS Equus caballus (Horse).  
 OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
 OX NCBI\_TaxID=9796;  
 RN [1]  
 RP MEDLINE=20181263; PubMed=10718335;  
 RA Mierdl M., Morton C.L., Danks M.K., Potter P.M.;  
 RT "Isolation and characterization of a cDNA encoding a horse liver  
 butyrylcholinesterase: evidence for CPT-11 drug activation.";  
 RL Biochem. Pharmacol. 59: 773-781(2000).  
 CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.  
 DR EMBL; AF178685; AAF61480.1; -  
 DR HSP; P21836; INSM.  
 DR GO; GO:0004104; F:cholinesterase activity; IEA.  
 DR GO; GO:0016787; F:hydrolase activity; IEA.  
 DR InterPro; IPR002018; CarbestereaseB.  
 DR InterPro; IPR000979; Cholinesterase.  
 DR InterPro; IPR000379; Ser\_estr.  
 DR Pfam; PF00135; Coesterase; 1.  
 DR PRINTS; PR00878; CHOLINESTRASE.  
 DR PROSITE; PS00122; CARBOXYLESTERASE\_B\_1; 1.  
 DR PROSITE; PS00941; CARBOXYLESTERASE\_B\_2; 1.  
 KW Hydrolase.  
 SQ SEQUENCE 602 AA; 68838 MW; 94C73F00431DF26E CRC64;  
 Query Match 87.7%; Score 2858; DB 2; Length 602;  
 Best Local Similarity 89.6%; Pred. No. 1.6e-206; Matches 537; Conservative 20; Mismatches 42; Indels 0; Gaps 0;

```

QY 301 LLINEAFVVPYGTPLSVNFGPTVDGFLTMDPDLLELZGPKKTOILVGNKDEGTWFLVY 360
DB 301 LLINEAFVVPYGTPLSVNFGPTVDGFLTMDPDLLELZGPKKTOILVGNKDEGTWFLVY 360
QY 361 GARPFSKDNNSIITRKEFGGLKIFFPGVSEFGKESILFFHTYWDVDORPENYREALGV 420
DB 361 GARPFSKDNNSIITRKEFGGLKIFFPGVSEFGKESILFFHTYWDVDORPENYREALGV 420
QY 421 VGDNVFCPLLEFKKSEWGNNAFFYYFEHRSSKLPWPMWGMVMEGYELIEFVGLPLER 480
DB 421 VGDNVFCPLLEFKKSEWGNNAFFYYFEHRSSKLPWPMWGMVMEGYELIEFVGLPLER 480
QY 481 RDNTYKAEBILSRISIVKRWANFAKYGNPNSTONNSISWVFKSTEOKYLTLNSTRINT 540
DB 481 RDNTYKAEBILSRISIVKRWANFAKYGNPNSTONNSISWVFKSTEOKYLTLNSTRINT 540
QY 541 KLRAGQOCRFWTLFFPKVLELTGNIDEAREWKAGFHRNNYMDMKQFNDYTSKES 599
DB 541 KLRAGQOCRFWTLFFPKVLELTGNIDEAREWKAGFHRNNYMDMKQFNDYTSKES 599

RESULT 3
CHLE_RABIT STANDARD; PRT; 581 AA.
ID CHLE_RABIT STANDARD; PRT; 581 AA.
AC P21927;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Cholinesterase precursor (EC 3.1.1.8) (acetylcholine acylhydrolase)
DE (Choline esterase II) (Butyrylcholine esterase)
DE (Pseudocholesterase).
DE Name=BCH;
OS Oryctolagus cuniculus (Rabbit).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OC NCBI_TaxId=9986;
OX 11
RX STRAIN=New Zealand;
RX MEDLINE=90326526; PubMed=2374720;
RA "Jbilo O., Roudani S., Chatonnet A.;
RT "Complete sequence of rabbit butyrylcholinesterase.";
RL Nucleic Acids Res. 18:3990-3990(1990).
RN 12
RP SEQUENCE OF 75-215 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=91201348; PubMed=2016308;
RA Arpagaus M., Chatonnet A., Masson P., Newton M., Vaughan T.A.,
RT Barthele C.F., Nogueira C.P., la Du B.N., Lockridge O.;
RT "Use of the polymerase chain reaction for homology probing of
RL butyrylcholinesterase from several vertebrates.";
RT J. Biol. Chem. 266:6966-6974(1991).
CC -1- CATALYTIC ACTIVITY: An acylcholine + H(2)O = choline + a
CC carboxylic acid anion.
CC -1- SUBUNIT: Homotetramer. The tetramer is composed of two dimers. The
CC two subunits in a dimer are linked by a disulfide bond.
CC -1- TISSUE SPECIFICITY: Present in most cells except erythrocytes.
CC -1- MISCELLANEOUS: Cholinesterase is highly reactive with
CC organophosphate esters.
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC
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CC
CC EMBL; X52090; CAA36308.1; -
CC EMBL; X52091; CAA36308.1; JOINED.
CC EMBL; X52092; CAA36308.1; JOINED.

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DR EMBL; M62779; AAA31169.1; -
DR PIR; S10255; C39768.
DR HSSP; P2303; 1F8U. Carbesteraeb.
DR InterPro; IPR002018; Cholinesterase.
DR InterPro; IPR000379; Ser_estr.
DR Pfam; PF00135; Coesterase; 1.
DR PRINTS; PR00678; CHOLINESTRAS.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
DR PROSITE; PS00941; Serine esterase; Signal.
KW Glycoprotein; Hydrolase; Signal.
FT SIGNAL 1
FT CHAIN 1
FT ACT_SITE 205 205
FT ACT_SITE 332 332
FT ACT_SITE 445 445
FT DISULFID 72 99
FT DISULFID 259 270
FT DISULFID 407 526
FT DISULFID 578 578
FT CARBOHYD 113 113
FT CARBOHYD 248 248
FT CARBOHYD 263 263
FT CARBOHYD 348 348
FT CARBOHYD 462 462
FT CARBOHYD 488 488
FT CARBOHYD 492 492
FT CARBOHYD 493 493
SQ SEQUENCE 581 AA; 66156 MW; F8B199F7B32EB0A CMC64;

Query Match 87.6%; Score 2855.5; DB 1; Length 581;
Best Local Similarity 91.4%; Pred. No. 2.3e-206;
Matches 531; Conservative 12; Mismatches 37; Indels 1; Gaps 1;

QY 21 MLIGKSHEDDITATKTKKVGKMLTVFGGVVTAFLGIPYAOPLGLRPRKPOSTLTKW 80
DB 1 MYRRSHTB-DVITTKNKRIRGINLPVFGGVVTAFLGIPYAOPLGLRPRKPOSTLTKW 59
QY 81 SDIWNATKYANCCCNIDDSFPFGSEWMMNENTLSEDCLYLNVWIPAPKRNATVLIV 140
DB 60 SDIWNATKYANCCCNIDDSFPFGSEWMMNENTLSEDCLYLNVWIPAPKRNATVLIV 119
QY 141 IYGGGFQGTSSLHAYVDGKFLARVERIVVSNVYVAGLGFALNGNBEAPNMGLPQQ 200
DB 120 IYGGGFQGTSSLHAYVDGKFLARVERIVVSNVYVAGLGFALNGNBEAPNMGLPQQ 179
QY 201 LALOWOKNINAARGNPKSVTLFGESAGAASVLSHLSPGSHLFTRALIQQSFPNAPWA 260
DB 180 LALOWOKNINAARGNPKSVTLFGESAGAASVLSHLSPGSHLFTRALIQQSFPNAPWA 239
QY 261 VTSIYKARNNTLNAKLTGCSRENTEYIKCLRNDKPOEILNEAFVVPYGTPLSVNFGP 320
DB 240 VMSIHEARNRTLTLAFVVGCGSTENETIICKLRNDKPOEILNEAFVVPYGTPLSVNFGP 299
QY 321 TVDGDPLTMDPDLLELZGPKKTOILVGNKDEGTWFLVYAGPFSKDNNSIITRKEFOE 380
DB 300 TVDGDPLTMDPDLLELZGPKKTOILVGNKDEGTWFLVYAGPFSKDNNSIITRKEFOE 359
QY 381 GLKIFPGVSEFGKESILFFHTYWDVDORPENYREALGVGDYNYFCPLLEFKKSEW 440
DB 360 GLKIFPGVSEFGKESILFFHTYWDVDORPENYREALGVGDYNYFCPLLEFKKSEW 419
QY 441 GNNAFYYFEHRSSKLPWPMWGMVMEGYELIEFVGLPLERDNTYKAEBILSRISIVKRW 500
DB 420 GNNAFYYFEHRSSKLPWPMWGMVMEGYELIEFVGLPLERDNTYKAEBILSRISIVKRW 479
QY 501 NFATYGNPNSTONNSISWVFKSTEOKYLTLNSTRINTKLRAGQOCRFWTLFFPKVLE 560
DB 480 NFATYGNPNSTONNSISWVFKSTEOKYLTLNSTRINTKLRAGQOCRFWTLFFPKVLE 539
QY 561 TGNIDEAREWKAGFHRNNYMDMKQFNDYTSKESCVG 601

```

Db 540 TGNIDEAEQEWKAGFHRMNNYMMAMKNNFNDYTSKERCAG 560

## RESULT 4

CHIE\_FELCA STANDARD; PRT; 602 AA.

AC 062760;  
 DT 29-MAR-2004 (Rel. 43, Created)  
 DT 29-MAR-2004 (Rel. 43, Last sequence update)  
 DT 01-OCT-2004 (Rel. 45, Last annotation update)  
 DE Cholinesterase precursor (EC 3.1.1.8) (Acetylcholine acylhydrolase)  
 DE (Choline esterase II) (Butyrylcholine esterase)  
 DE (Pseudocholinesterase).  
 GN Name=BCH;  
 OS Felis silvestris catus (Cat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Placentalia; Felidae; Felis.  
 OK NCBI\_TaxID=9685;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Pituitary;  
 RX MEDLINE=20334351; PubMed=10874122;  
 RA Bartels C.F., Xie W., Miller-Lindholm A.K., Schopfer L.M.,  
 Lockridge O.;  
 RT "determination of the DNA sequences of acetylcholinesterase and  
 RT butyrylcholinesterase from cat and demonstration of the existence of  
 RT both in cat plasma."  
 RL Biochem. Pharmacol. 60:479-487(2000).  
 CC -1- CATALYTIC ACTIVITY: An acylcholine + H(2)O = choline + a  
 CC carboxylic acid anion.  
 CC -1- SUBUNIT: Homotetramer. The tetramer is composed of two dimers. The  
 CC two subunits in a dimer are linked by a disulfide bond (By  
 CC similarity).  
 CC -1- MISCELLANEOUS: Cholinesterase is highly reactive with  
 CC organophosphate esters (By similarity).  
 CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL: AF053483; AAC06261.1; -.  
 DR HSP; P22303; IBA1.  
 DR InterPro: IPR002018; CarbesteraseB.  
 DR InterPro: IPR000997; Cholinesterase.  
 DR InterPro: IPR000379; Ser ests.  
 DR Pfam: PF00135; Coesterase\_1.  
 DR PRINTS; PR00878; CHOLNSTRASE.  
 DR PROSITE; PS00122; CARBOXYLESTERASE\_B\_1; 1.  
 DR PROSITE; PS00941; CARBOXYLESTERASE\_B\_2; 1.  
 KW Glycoprotein; Hydrolase; Serine esterase; Signal.  
 FT SIGNAL 1 28  
 FT CHAIN 29 602  
 FT ACT\_SITE 226 602  
 FT ACT\_SITE 353 353  
 FT ACT\_SITE 466 466  
 FT DISULFID 93 120  
 FT DISULFID 280 291  
 FT DISULFID 428 547  
 FT DISULFID 599 599  
 FT CARBOHYD 85 85  
 FT CARBOHYD 134 134  
 FT CARBOHYD 269 269  
 FT CARBOHYD 284 284  
 FT CARBOHYD 369 369  
 FT CARBOHYD 483 483  
 FT CARBOHYD 509 509  
 FT CARBOHYD 513 513  
 FT CARBOHYD 514 514

SO SEQUENCE 602 AA; 68328 MW; ECB8879232B74B9C CRC64;

Query Match 85.4%; Score 2784; DB 1; Length 602;  
 Best Local Similarity 86.9%; Pred. No. 6e-201;  
 Matches 523; Conservative 24; Mismatches 55; Indels 0; Gaps 0;

QY 1 MDSKVTITICIRPLFWILLCLMIGKSHTEDDIIATKNGKVRGNTLVFGYTAFFGIP 60  
 DB 1 MOSKGTIISIFLIRFLWLVIGKSHTEDDIIITKNGKVRGNTLVFGYTAFFGIP 60  
 QY 61 YAOPIGRLEFRKPKQSLTKMSDIWNATKYNSCCONIDSPFPFSEMMNPMTDSEDC 120  
 DB 61 YAOPIGRLEFRKPKQSLTKMSDIWNATKYNSCYQNAQSPFPFSEMMNPMTDSEDC 120  
 QY 121 LYANVMIPAKPKNAATVLIWYGGFOTGSSLIHVDGKLAVERIVVSMNVYVAGLG 180  
 DB 121 LYANVMIPAKPKNAATVLIWYGGFOTGSSLIHVDGKLAVERIVVSMNVYVAGLG 180  
 QY 181 FLALPQNPAPNGMGLFDQGLALQWYQKNTAFQGNPKSVTLFGESAGAAVSILHLSPG 240  
 DB 181 FLALPQNPAPNGMGLFDQGLALQWYQKNTAFQGNPKSVTLFGESAGAAVSILHLSPG 240  
 QY 241 SHSLFTRAILQSSGFAPAAVTSIYERARTLALATGSRNEMETIICLNKPOEI 300  
 DB 241 SHSLFTRAILQSSGFAPAAVTSIYERARTLALATGSRNEMETIICLNKPOEI 300  
 QY 301 LLINEAFVPGYPTPLSVNFGPTVDGDFLTMDPDLLEIGQPKTQILVGVKDEGTWFLV 360  
 DB 301 LLINEAFVPGYPTPLSVNFGVVDGDFLTMDPDLLEIGQPKTQILVGVKDEGTWFLV 360  
 QY 361 GARGFSKDNNSITTRKFOGKIFPPGVSEPKESILFHYTWDVDDQRPENTREALGV 420  
 DB 361 GARGFSKDNNSITTRKFOGKIFPPGVSEPKESILFHYTWDVDDQRPENTREALGV 420  
 QY 421 VGVNFIICPLLETTKTFSEWGNNAFFPYFHRSSKLPWPMWVMGYELFPGPLER 480  
 DB 421 VGVNFIICPLLETTKTFSEWGNNAFFPYFHRSSKLPWPMWVMGYELFPGPLER 480  
 QY 481 RDVYTKAEILISIVKMANFAKYGNPETQNNSTWPFKSTEOXYTLTNTSTRTMT 540  
 DB 481 RDVYTKAEILISIVKMANFAKYGNPETQNNSTWPFKSTEOXYTLTNTSTRTMT 540  
 QY 541 KLRAGQCRFTSFPFVLEMTGNIDEAEWEMKAGFHRMNNYMMAMKNNFNDYTSKESCV 600  
 DB 541 KLRAGQCRFTSFPFVLEMTGNIDEAEWEMKAGFHRMNNYMMAMKNNFNDYTSKESCA 600  
 QY 601 GL 602  
 DB 601 GL 602

## RESULT 5

CHIE\_HORSE STANDARD; PRT; 574 AA.

AC P81908;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 01-OCT-2004 (Rel. 45, Last annotation update)  
 DE Cholinesterase (EC 3.1.1.8) (Acetylcholine acylhydrolase) (Choline  
 DE esterase II) (Butyrylcholine esterase) (Pseudocholinesterase) (Eq-  
 DE BCHB).  
 GN Name=BCHB;  
 OS Equus caballus (Horse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
 OK NCBI\_TaxID=9796;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Plasma;  
 RA Moorad D.R., Luo C., Garcia G.B., Doctor B.P.;  
 RT "Amino acid sequence of horse serum butyrylcholinesterase."  
 RL (in) Doctor B.P., Taylor P., Quinn D.M., Rotundo R.L., Gentry M.K.  
 (eds.);

RL Structure and function of cholinesterases and related proteins,  
 RL pp.145-146, Plenum Press, New York and London (1998).  
 CC -1- CATALYTIC ACTIVITY: An acylcholine + H(2)O = choline + a  
 CC carboxylic acid anion.  
 CC -1- SUBUNIT: Homotetramer. The tetramer is composed of two dimers. The  
 CC two subunits in a dimer are linked by a disulfide bond.  
 CC -1- TISSUE SPECIFICITY: Present in most cells except erythrocytes.  
 CC -1- MISCELLANEOUS: Cholinesterase is highly reactive with  
 CC organophosphate esters.  
 CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.  
 CC HSSP; P21836; INSM.  
 DR InterPro: IPR002018; CarpesteraseB.  
 DR InterPro: IPR000997; Cholinesterase.  
 DR InterPro: IPR000379; Ser\_ests.  
 DR Pfam: PF00135; Coesterase\_1.  
 DR PRINTS; PR00878; CHOLNSTRASE.  
 DR PROSITE; PS00122; CARBOXYLESTERASE\_B\_1; 1.  
 DR PROSITE; PS00941; CARBOXYLESTERASE\_B\_2; 1.  
 KM Direct protein sequencing: Glycoprotein; Hydrolase; Serine esterase.  
 FT ACT\_SITE 198 198 Acyl-ester intermediate (By similarity).  
 FT ACT\_SITE 325 325 Charge relay system (By similarity).  
 FT ACT\_SITE 438 438 Charge relay system (By similarity).  
 FT ACT\_SITE 438 438 Charge relay system (By similarity).  
 FT DISULFID 252 263 By similarity.  
 FT DISULFID 400 519 By similarity.  
 FT DISULFID 571 571 Interchain (By similarity).  
 FT CARBOHYD 57 57 N-linked (GlcNAc...).  
 FT CARBOHYD 106 106 N-linked (GlcNAc...).  
 FT CARBOHYD 241 241 N-linked (GlcNAc...).  
 FT CARBOHYD 256 256 N-linked (GlcNAc...).  
 FT CARBOHYD 341 341 N-linked (GlcNAc...).  
 FT CARBOHYD 445 445 N-linked (GlcNAc...).  
 FT CARBOHYD 481 481 N-linked (GlcNAc...).  
 FT CARBOHYD 486 486 N-linked (GlcNAc...).  
 SQ SEQUENCE 574 AA; 65641 MW; 07755E9FB9CB3E CRC64;  
 Query Match 85.1%; Score 2774; DB 1; Length 574;  
 Best Local Similarity 90.5%; Pred. No. 3,2e-200;  
 Matches 517; Conservative 20; Mismatches 34; Indels 0; Gaps 0;

DB 481 NETONNSTSMWPFVFKSTBQKYLTLNTESTRIWTKLRAQCCRFWTLEFPVLEMTGNIDAE 540  
 QY 569 WEKXAGFHRNNYMMNDKNOFNDYTSKESC 599  
 DB 541 REMKAGFHRNNYMMNDKNOFNDYTSKESC 571  
 RESULT 6  
 CHIE\_PANTT STANDARD; PRT; 602 AA.  
 ID CHIE\_PANTT  
 AC 062761;  
 DT 29-MAR-2004 (Rel. 43, Created)  
 DT 29-MAR-2004 (Rel. 43, Last sequence update)  
 DT 01-OCT-2004 (Rel. 45, Last annotation update)  
 DE Cholinesterase precursor (EC 3.1.1.8) (Acylcholine acylhydrolase)  
 DE (choline esterase II) (Butyrylcholine esterase)  
 DE (pseudocholinesterase).  
 GN Name=BCH;  
 OS Panthera tigris tigris (Bengal tiger).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Panthera.  
 OX NCBI\_TaxID=7435;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Plutary;  
 RX MEDLINE=20334351; PubMed=10874122;  
 RA Bartels C.R., Xie W., Miller-Lindholm A.K., Schopfer L.M.,  
 RA Lockridge O.;  
 RT "Determination of the DNA sequences of acetylcholinesterase and  
 RT butyrylcholinesterase from cat and demonstration of the existence of  
 RT both in cat plasma."  
 RL Biochem. Pharmacol. 60:479-487(2000).  
 CC -1- CATALYTIC ACTIVITY: An acylcholine + H(2)O = choline + a  
 CC carboxylic acid anion.  
 CC -1- SUBUNIT: Homotetramer. The tetramer is composed of two dimers. The  
 CC two subunits in a dimer are linked by a disulfide bond (By  
 CC similarity).  
 CC -1- MISCELLANEOUS: Cholinesterase is highly reactive with  
 CC organophosphate esters (By similarity).  
 CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; AF053484; AAC06262.1; -.  
 CC HSSP; P22303; 1B41.  
 DR InterPro: IPR002018; CarpesteraseB.  
 DR InterPro: IPR000997; Cholinesterase.  
 DR InterPro: IPR000379; Ser\_ests.  
 DR Pfam; PF00135; Coesterase\_1.  
 DR PRINTS; PR00878; CHOLNSTRASE.  
 DR PROSITE; PS00122; CARBOXYLESTERASE\_B\_1; 1.  
 DR PROSITE; PS00941; CARBOXYLESTERASE\_B\_2; 1.  
 DR Glycoprotein; Hydrolase; Serine esterase; signal.  
 KW SIGNAL 1 28  
 FT CHAIN 29 602  
 FT ACT\_SITE 226 226 Cholinesterase.  
 FT ACT\_SITE 353 353 Acyl-ester intermediate (By similarity).  
 FT ACT\_SITE 466 466 Charge relay system (By similarity).  
 FT DISULFID 93 120 Charge relay system (By similarity).  
 FT DISULFID 280 291 By similarity.  
 FT DISULFID 428 547 By similarity.  
 FT DISULFID 599 599 Interchain (By similarity).  
 FT CARBOHYD 85 85 N-linked (GlcNAc...).  
 FT CARBOHYD 134 134 N-linked (GlcNAc...).  
 FT CARBOHYD 269 269 N-linked (GlcNAc...).  
 FT CARBOHYD 284 284 N-linked (GlcNAc...).  
 FT CARBOHYD 284 284 N-linked (GlcNAc...).

FT CARBOHYD 369 369 N-linked (GlcNAc. . .) (Potential).  
 FT CARBOHYD 483 483 N-linked (GlcNAc. . .) (Potential).  
 FT CARBOHYD 509 509 N-linked (GlcNAc. . .) (Potential).  
 FT CARBOHYD 513 513 N-linked (GlcNAc. . .) (Potential).  
 FT CARBOHYD 514 514 N-linked (GlcNAc. . .) (Potential).  
 SQ SEQUENCE 602 AA; 68289 MW; EB0CB9148B956A1 CRC64;

Query Match 85.0%; Score 2772; DB 1; Length 602;  
 Best Local Similarity 86.5%; Pred. No. 4,8e-200;  
 Matches 521; Conservative 25; Mismatches 56; Indels 0; Gaps 0;

QY 1 MDKATVITICRFLFWFLILCMKLGKSHTEDDIIATNGKRGKMLTVFGSTVAFGIP 60  
 DB 1 MOSKGTIISIOFLRFLRLWLIKSHTEBDIIITTKGKRGKMLPLDGTVAFAFGIP 60

QY 61 YAOPLRLRPRKPKOSITKMSDINNAKYNASCONIDQSPFGHSEMMNPNTDLSBDC 120  
 DB 61 YAOPLRLRPRKPKOSITKMSDINNAKYNASCONIDQSPFGHSEMMNPNTDLSBDC 120

QY 121 LYLWMTLPARKKATVLIWYGGGFGTGTSSLHVYDGKFLARVERVIVSMYRVGALG 180  
 DB 121 LYLWMTLPARKKATVLIWYGGGFGTGTSSLHVYDGKFLARVERVIVSMYRVGALG 180

QY 181 FLALPBNPEAGNGLFDQOLALQWQKNIAPFGSNPKSVTLFGESAGASVSLHLSPG 240  
 DB 181 FLALPBNPEAGNGLFDQOLALQWQKNIAPFGSNPKSVTLFGESAGASVSLHLSPR 240

QY 241 SHSLFTALIOSGSGFNAPMAVTSIYEARNRTLAKLTGCRNEMETIKLARKDPOEI 300  
 DB 241 SHSLFTALIOSGSGFNAPMAVTSIYEARNRTLAKLTGCRNEMETIKLARKDPOEI 300

QY 301 LLINEAFVVPYGTPTSVNFGPTVDGFLTMDPDLLEFGFKTQILVGNVDEGTWFLVY 360  
 DB 301 LLINEAFVVPYGTPTSVNFGPTVDGFLTMDPDLLEFGFKTQILVGNVDEGTWFLVY 360

QY 361 GAGFSGKDNNSITIRKKEFGELKIFPGVSEFGKESILFHTYDWDQRPENYREALGDV 420  
 DB 361 GAGFSGKDNNSITIRKKEFGELKIFPGVSEFGKESILFHTYDWDQRPENYREALGDV 420

QY 421 VGDVNFICPALFEPKKSSEMNNAFFYFHEHRSKLTWPEMGMGMGEGIEFVGLER 480  
 DB 421 VGDVNFICPALFEPKKSSEMNNAFFYFHEHRSKLTWPEMGMGMGEGIEFVGLER 480

QY 481 RDNVTKAEELISRSIVKMANFAKYGKPNETONNSTMPVKESTEOXYLTINTESTRIMT 540  
 DB 481 RDNVTKAEELISRSIVKMANFAKYGKPNETONNSTMPVKESTEOXYLTINTESTRIMT 540

QY 541 KLRAGQCRFWTSPFKYLEMTGNIDAEWEWKAQFHRMNNYMDWKQCFNDYTSKESCV 600  
 DB 541 KLRAGQCRFWTSPFKYLEMTGNIDAEWEWKAQFHRMNNYMDWKQCFNDYTSKESCV 600

QY 601 GL 602  
 DB 601 GL 602

RESULT 7  
 BAC34196 PRELIMINARY; PRT; 603 AA.  
 AC BAC34196;  
 DT 14-APR-2004 (TREMblrel. 27, Created)  
 DT 14-APR-2004 (TREMblrel. 27, Last sequence update)  
 DE 14-APR-2004 (TREMblrel. 27, Last annotation update)  
 DE Adult male liver tumor cdna, RIKEN full-length enriched library,  
 DE clone: C730038G20 product: Ductylcholesterase.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Liver;  
 RX MEDLINE=22354683; PubMed=1246851;

RA The FANTOM Consortium,  
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs.";  
 RL Nature 420:563-573(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Liver;  
 RX MEDLINE=21085660; PubMed=11217851;  
 RA RIKEN FANTOM Consortium;  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690(2001).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Liver;  
 RX MEDLINE=99279253; PubMed=103463636;  
 RA Carninci P., Hayashizaki Y.,  
 RT "High-efficiency full-length cDNA cloning.";  
 RL Meth. Enzymol. 303:19-44(1999).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Liver;  
 RX MEDLINE=20493374; PubMed=11042159;  
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,  
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";  
 RL Genome Res. 10:1617-1630(2000).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Liver;  
 RX MEDLINE=20530913; PubMed=11076861;  
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
 RA Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,  
 RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
 RA Yamamoto R., Matsuno H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,  
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,  
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,  
 RT "RIKEN integrated sequence analysis (RISA) system-384-format  
 RT sequencing pipeline with 384 multiplexed capillary sequencer.";  
 RL Genome Res. 10:1757-1771(2000).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Liver;  
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
 RA Fukuda S., Furuno M., Hamaguchi T., Hara A., Hashizume W.,  
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozawa T.,  
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,  
 RA Kuribara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,  
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,  
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,  
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL, AK050337; BAC34196.1; -;  
 SQ SEQUENCE 603 AA; 68462 MW; 2CB79C4679B3713 CRC64;

Query Match 79.8%; Score 2602; DB 2; Length 603;  
 Best Local Similarity 80.5%; Pred. No. 3.1e-187;  
 Matches 476; Conservative 47; Mismatches 68; Indels 0; Gaps 0;

QY 12 PLFWFLILCMKLGKSHTEDDIIATNGKRGKMLTVFGSTVAFGIPPAOPLGLR 71  
 DB 13 FLIMILILCMKLPFGKSHTEBFIITTKGVRGKSMVVLGGTVAFAGIPPAOPLGLR 72

QY 72 KKPOSLTKMSDINNAKYNASCONIDQSPFGHSEMMNPNTDLSBDCILYLVMTLPARK 131  
 DB 73 KKPOSLTKMSDINNAKYNASCONIDQSPFGHSEMMNPNTDLSBDCILYLVMTLPARK 132

QY 132 PKNATVLIWYGGGFGTGTSSLHVYDGKFLARVERVIVSMYRVGALGPLAPNPEAP 191



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Db      133 PKNATVWVWYGGGFGTSSLPVYDGKFLARVERIVVSMYRVGALGFLAPGNDPAP 192
Qy      192 GNMGLFPQOALQWVQKNIAAFGNGPKSVTLFGESGAASVSLHLLSPGSHLFTRAIQ 251
Db      193 GNMGLFPQOALQWVQKNIAAFGNGPKSVTLFGESGAASVSLHLLCPQSYLFTRAIQ 252
Qy      252 SSGSNAPWATVSYEAARNTLAKLTGCSRENTEITIKLRNKDQOELLNEAFVVPYG 311
Db      253 SSGSNAPWATVSYEAARNTLAKLTGCSRENTEITIKLRNKDQOELLNEAFVVPYG 312
Qy      312 TPLSVNGPVTVDGFLTDMEDILLETGQFKKTQILVGVNDEGTWFLVYGAPEFSKDNDS 371
Db      313 SILSINFGPVTVDGFLTDMEDILLETGQFKKTQILVGVNDEGTWFLVYGAPEFSKDNDS 372
Qy      372 IITKEPQEGIKTFPPVSEFGKESILFHYTDVWDQRPENYEAALGDVVDGYNFICPAL 431
Db      373 LITKEPQEGIKTFPPVSEFGKESILFHYTDVWDQRPENYEAALGDVVDGYNFICPAL 432
Qy      432 EFTKKFSEMGNNAPFFYFEHRSKLPWEMWGVHGEIEFVGLPLERDNTTKAEIL 491
Db      433 EFTKKFSEMGNNAPFFYFEHRSKLPWEMWGVHGEIEFVGLPLERDNTTKAEIL 492
Qy      492 SRSIYKRWANPAKYGNEPMTQNSTWVPFKSTOKLTLNTESTRITMTKLPAQOCRFMT 551
Db      493 SRSIYKRWANPAKYGNEPMTQNSTWVPFKSTOKLTLNTESTRITMTKLPAQOCRFMT 552
Qy      552 SFPFKVLTMTGNIDAEWEMKAGFHRNNVMDKNOFNDYTSKESCVGL 602
Db      553 LFPFKVLTMTGNIDAEWEMKAGFHRNNVMDKNOFNDYTSKESCVGL 603

```

## RESULT 8

CHLE MOUSE STANDARD; PRT; 603 AA.

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AC 00311:
ID CHLE MOUSE STANDARD; PRT; 603 AA.
AC 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Cholinesterase precursor (EC 3.1.1.8) (Acylcholine acylhydrolase)
DE (Choline esterase II) (Butyrylcholine esterase)
DE (Pseudochoolinesterase).
CN Name:Boche;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90380429; PubMed=2400605;
RA Rachinsky T.L., Camp S., Li Y., Ekstrom T.J., Newton M., Taylor P.;
RT "Molecular cloning of mouse acetylcholinesterase: tissue distribution
RT of alternatively spliced mRNA species.";
RL Neuron 5:317-327(1990).
RN [2]
RP SEQUENCE OF 97-237 FROM N.A.
RC TTSUB=Liver;
RX MEDLINE=91201348; PubMed=2016308;
RA Arpaia M., Chatonnet A., Masson P., Newton M., Vaughan T.A.,
RA Bartels C.F., Nogueira C.P., La Du B.N., Lockridge O.;
RT "Use of the polymerase chain reaction for homology probing of
RT butyrylcholinesterase from several vertebrates.";
RL J. Biol. Chem. 266:6966-6974(1991).
RL J. Biol. Chem. 266:6966-6974(1991).
CC -1- CATALYTIC ACTIVITY: An acylcholine + H(2)O = choline + a
CC carboxylic acid anion.
CC -1- SUBUNIT: Homotetramer. The tetramer is composed of two dimers. The
CC two subunits in a dimer are linked by a disulfide bond.
CC -1- TISSUE SPECIFICITY: Present in most cells except erythrocytes.
CC -1- MISCELLANEOUS: Cholinesterase is highly reactive with
CC organophosphate esters.
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC -----
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DR EMBL: M99492; AAA37328.1; --
DR PIR: S70849; S70849.
DR HSSP: P22303; 198U.
DR MGI: MGI:894278; Bcne.
DR InterPro: IPR002018; CarbestereaseB.
DR InterPro: IPR000997; Cholinesterase.
DR InterPro: IPR00379; Ser ester.
DR Pfam: PF00135; Coesterase; 1.
DR PRINTS: PR00878; CHOLINESTRASE.
DR PROSITE: PS00122; CARBOXYL-ESTERASE_B_1; 1.
DR PROSITE: PS00941; CARBOXYL-ESTERASE_B_2; 1.
DR GlycoProtein; Hydrolyase; Serine esterase; Signal.
KW SIGNAL
FT CHAIN 1 29
FT ACT_SITE 30 603
FT ACT_SITE 227 227
FT ACT_SITE 354 354
FT ACT_SITE 467 467
FT DISULFID 94 121
FT DISULFID 281 292
FT DISULFID 429 548
FT DISULFID 600 600
FT CARBOHYD 86 86
FT CARBOHYD 135 135
FT CARBOHYD 270 370
FT CARBOHYD 370 370
FT CARBOHYD 484 484
FT CARBOHYD 510 510
FT CARBOHYD 515 515
FT CONFLICT 129 129
SQ SEQUENCE 603 AA; 68521 MW; 719B1B220D1E5367 CRC64;

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Query Match 79.5%; Score 2593; DB 1; Length 603;  
Best Local Similarity 80.4%; Pred. No. 1.5e-186;  
Matches 475; Conservative 47; Mismatches 69; Indels 0; Gaps 0;

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Qy 12 FLFWPLLLGKSTEDDIIATKNGKVRGMLTVGTVTAFIPIYAPQPLGRURF 71
Db 13 FLFWPLLLGKSTEDDIIATKNGKVRGMLTVGTVTAFIPIYAPQPLGRURF 72
Qy 72 KKPQSLTKNSDINWATKYANSCCQNDISFPGHSGEMNPTDISEDCLYANWTPAK 131
Db 73 KKPQSLTKNSDINWATKYANSCCQNDISFPGHSGEMNPTDISEDCLYANWTPAK 132
Qy 132 PKNATVWVWYGGGFGTSSLPVYDGKFLARVERIVVSMYRVGALGFLAPGNDPAP 191
Db 133 PKNATVWVWYGGGFGTSSLPVYDGKFLARVERIVVSMYRVGALGFLAPGNDPAP 192
Qy 192 GNMGLFPQOALQWVQKNIAAFGNGPKSVTLFGESGAASVSLHLLSPGSHLFTRAIQ 251
Db 193 GNMGLFPQOALQWVQKNIAAFGNGPKSVTLFGESGAASVSLHLLCPQSYLFTRAIQ 252
Qy 252 SSGSNAPWATVSYEAARNTLAKLTGCSRENTEITIKLRNKDQOELLNEAFVVPYG 311
Db 253 SSGSNAPWATVSYEAARNTLAKLTGCSRENTEITIKLRNKDQOELLNEAFVVPYG 312
Qy 312 TPLSVNGPVTVDGFLTDMEDILLETGQFKKTQILVGVNDEGTWFLVYGAPEFSKDNDS 371
Db 313 SILSINFGPVTVDGFLTDMEDILLETGQFKKTQILVGVNDEGTWFLVYGAPEFSKDNDS 372
Qy 372 IITKEPQEGIKTFPPVSEFGKESILFHYTDVWDQRPENYEAALGDVVDGYNFICPAL 431
Db 373 LITKEPQEGIKTFPPVSEFGKESILFHYTDVWDQRPENYEAALGDVVDGYNFICPAL 432
Qy 432 EFTKKFSEMGNNAPFFYFEHRSKLPWEMWGVHGEIEFVGLPLERDNTTKAEIL 491
Db 433 EFTKKFSEMGNNAPFFYFEHRSKLPWEMWGVHGEIEFVGLPLERDNTTKAEIL 492

```



QY 492 SRSIVKMANFAXYGNPNETONNSTSWPVFKSTBOXYLLTNTESRITMTKLRPAOQCRFWT 551  
 DB 493 SRSIMKTWANFAXYGNPNETONNSTSWPVFKSTBOXYLLTNTESRITMTKLRPAOQCRFWT 552  
 QY 552 SFPKPVLEMTGNIDEAEWEMKAGFHRNNYMMDMKNOFNNDYTSKKEGCVL 602  
 DB 553 LFPKPVLEMTGNIDEAEWEMKAGFHRNNYMMDMKNOFNNDYTSKKEGCVL 603

## RESULT 9

090KCI PRELIMINARY; PRT; 597 AA.  
 ID Q90KCI  
 AC Q90KCI; 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DE Butyrylcholinesterase.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Heart;  
 RA Tieu A.M., Lockridge O., Bartels C.F.;  
 RA Li B., Scribley J., Tieu A., Xie W., Schopfer L.M., Hammond P.,  
 RA Brimljoin S., Hnrichs S.H., Lockridge O.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Heart;  
 RA Tieu A.M., Lockridge O., Bartels C.F.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.  
 DR EMBL: AF244349; AAF4713.1; -.  
 DR HSBP; P23203; 1F8U.  
 DR GO; GO:0003824; F:catalytic activity; IEA.  
 DR GO; GO:0004104; F:cholinesterase activity; IEA.  
 DR InterPro: IPR002018; CarbesteraseB.  
 DR InterPro: IPR000997; Cholinesterase.  
 DR InterPro: IPR000379; Ser\_estrs.  
 DR Pfam; PF00135; Coesterase; 1.  
 DR PRINTS; PR00878; CHOLNSTRASE.  
 DR PROSITE; PS00122; CARBOXYLESTERASE\_B\_1; 1.  
 DR PROSITE; PS00941; CARBOXYLESTERASE\_B\_2; 1.  
 KW Hydrolase.  
 SQ SEQUENCE 597 AA; 67776 MW; 771204D166C7BEAC CRC64;

Query Match 79.4%; Score 2588; DB 2; Length 597;  
 Best Local Similarity 79.8%; Pred. No. 3.5e-186;  
 Matches 473; Conservative 47; Mismatches 73; Indels 0; Gaps 0;

QY 10 IRPLFWLLLCMLIGKSHTEDDIIATKNGKVRGNLTTFGCTVTAFLGIPYAOPPLGRL 69  
 DB 5 IHFLMTLLLCMLFGKSHTEDEVIITTKGVRGSLSPMILGGITVTAFLGIPYAOPPLGSL 64  
 QY 70 RPKKPOSLLTKMSDIWNAATKYANSCONIDOSFPGFHSSEMMNPNTDISEDCLYTNWIPA 129  
 DB 65 RPKKPOSLLTKMSDIWNAATKYANSCONIDOSFPGFHSSEMMNPNTDISEDCLYTNWIPA 124  
 QY 130 PKPKNATVLIWYGGFQGTGTSLSHVDGKFLAVERIVVSNMYRVGALGFLALPGNPE 189  
 DB 125 PKPKNATVLIWYGGFQGTGTSLSHVDGKFLAVERIVVSNMYRVGALGFLALPGNSE 184  
 QY 190 APGNGMGLPDQOLALQWQKNTAAFGNPKSYTLFGESAGAAVSLSHLSPSHSLFTRAI 249  
 DB 185 APGNGMGLPDQOLALQWQKNTAAFGNPKSYTLFGESAGAAVSLSHLSPSHSLFTRAI 244  
 QY 250 LOSGSPAPAPAVATSLYEARNRTLLAKLTLGCSRENTEFIIKCLNNKPOEILLNEAFVFP 309  
 DB 245 LBSGSSNAAPAVAKPEPARKRTLLAKFISGSKNEKEIITCLASKQPOEILLNEKVLFP 304  
 QY 310 YGTPLSVNFPGFTVDGFLTDMPIILLEGQPKTKQIILGVNKGEGTWFLVYGAFGFSKDN 369

DB 305 SDSIRSINFPPTVDGFLTDMPTLLQLGKCYAQAQIILGVNKGEGTAFVYGAFGFSKDN 364  
 QY 370 NSIITRKEPQGLKIPFGVSEFKESILFHYTDWDDQRPENYREALGVGDIYICP 429  
 DB 365 DSLITRKEPQGLKIPFGVSSIGKEALILFYTDWDDQRPENYREALGVGDIYICP 424  
 QY 430 ALBETTKFSEWGNNAFPYFPEHRSSKLPWPEWGMVHGVEIFVFGILPERRDNYTAER 489  
 DB 425 ALBETTKFSEWGNNAFPYFPEHRSSKLPWPEWGMVHGVEIFVFGILPERRDNYTAER 484  
 QY 490 ILSRSIVKMANFAXYGNPNETONNSTSWPVFKSTBOXYLLTNTESRITMTKLRPAOQCRF 549  
 DB 485 ILSRSIVKMANFAXYGNPNETONNSTSWPVFKSTBOXYLLTNTESRITMTKLRPAOQCRF 544  
 QY 550 WTSFPPVLEMTGNIDEAEWEMKAGFHRNNYMMDMKNOFNNDYTSKKEGCVL 602  
 DB 545 WTSFPPVLEMTGNIDEAEWEMKAGFHRNNYMMDMKNOFNNDYTSKKEGCVL 603

## RESULT 10

090ZK8 PRELIMINARY; PRT; 603 AA.  
 ID Q90ZK8  
 AC Q90ZK8; 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DE Butyrylcholinesterase precursor (EC 3.1.1.8).  
 GN Name-BCH;  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC Geisler K., Chatonnet A., Layer P.G.;  
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.  
 DR EMBL: AJ306328; CAC3792.1; -.  
 DR HSBP; P21836; 1NSM.  
 DR GO; GO:0004104; F:cholinesterase activity; IEA.  
 DR GO; GO:0016787; F:hydrolase activity; IEA.  
 DR InterPro: IPR002018; CarbesteraseB.  
 DR InterPro: IPR000997; Cholinesterase.  
 DR InterPro: IPR000379; Ser\_estrs.  
 DR Pfam; PF00135; Coesterase; 1.  
 DR PRINTS; PR00878; CHOLNSTRASE.  
 DR PROSITE; PS00122; CARBOXYLESTERASE\_B\_1; 1.  
 DR PROSITE; PS00941; CARBOXYLESTERASE\_B\_2; 1.  
 KW Hydrolase; Signal.  
 FT SIGNAL 1 29 Potential.  
 FT CHAIN 30 603 butyrylcholinesterase.  
 SQ SEQUENCE 603 AA; 68480 MW; A350PDD68574ADF CRC64;

Query Match 71.8%; Score 2339.5; DB 2; Length 603;  
 Best Local Similarity 71.9%; Pred. No. 1.9e-167;  
 Matches 427; Conservative 70; Mismatches 96; Indels 1; Gaps 1;

QY 8 ICIRPLFWLLLCMLIGKSHTEDDIIATKNGKVRGNLTTFGCTVTAFLGIPYAOPPLG 67  
 DB 9 ICARFLMTLLLCMLFMFIRKVPEDN-VITTEKGVRGTNLOVLGGITVTAFLGIPYKXPBG 67  
 QY 68 RLPKPOSLLTKMSDIWNAATKYANSCONIDOSFPGFHSSEMMNPNTDISEDCLYTNWIPA 127  
 DB 68 RLPKPOSLLTKMSDIWNAATKYANSCONIDOSFPGFHSSEMMNPNTDISEDCLYTNWIPA 127  
 QY 128 PAPKKNATVLIWYGGFQGTGTSLSHVDGKFLAVERIVVSNMYRVGALGFLALPGN 187  
 DB 128 PAPKKNATVLIWYGGFQGTGTSLSHVDGKFLAVERIVVSNMYRVGALGFLALPGN 187  
 QY 188 PEPNGMGLPDQOLALQWQKNTAAFGNPKSYTLFGESAGAAVSLSHLSPSHSLFTR 247  
 DB 188 PEPNGMGLPDQOLALQWQKNTAAFGNPKSYTLFGESAGAAVSLSHLSPSHSLFTR 247

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Db 188 KEVPGNAGLFDQRLALQWQENTASFGCNPKSVTTIGESAGASVSYHILSPKSHPLFR 247
Qy 248 AILQSGSFNAPMAVTSIYEARNRTNLAKLTCGSRNETEIIKCLRNKQPOBILNEAFV 307
Db 248 AILQSGSFNAPMAVTSIYEARNRTNLAKLTCGSRNETEIIKCLRNKQPOBILNEAFV 307
Qy 308 VPGTPLSVNPGFTVDGFLTMDPDLILBGOFRKQIILVGNVKDQSGMTLVYAGAPFK 367
Db 308 VKYFSLHIFCPVDVDFLADMEALIKGIFKQIVLVGNKDKSTSLVYGVGFSK 367
Qy 368 DNNISITRKEPOBGLKIFPGVSEFGKESILFHTYDWDVDDQRPENYREALGVVGYNFI 427
Db 368 DSDSLINKTQPERVALTISFPQVSKLAIESIIFQYTDWENQKPEHRDAMDVIGDYHII 427
Qy 428 CPALFTKKSSEWNNAPFYFIEHRSKSLPMEPMGMVGEIIEFVGLFLERDNYTKA 487
Db 428 CPVAFPAKTIAEVGNANVFYFIEHRSKSLPMEPMGMVGEIIEFVGLFLERDNYTKA 487
Qy 488 BEILSRSLVKNWAPAKYGNPNQNNSTSPVFKSTEOXYLTINTESTRIMTKLRAQOC 547
Db 488 BEILSRSLVKNWAPAKYGNPNQNNSTSPVFKSTEOXYLTINTESTRIMTKLRAQOC 547
Qy 548 RFTSPFKVLEMTGNIDAEEMWAGFHRNNNTMMQKQFNDYTSKKSQCVG 601
Db 548 RFTSPFKVLEMTGNIDAEEMWAGFHRNNNTMMQKQFNDYTSKKSQCVG 601
RESULT 11
ACES_ELEBL STANDARD; PRT; 633 AA.
ID ACES_ELEBL STANDARD; PRT; 633 AA.
AC 042275:
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Acetylcholinesterase precursor (EC 3.1.1.7) (AChE).
OS Electrophorus electricus (Electric eel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butelosteomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Gymnotiformes;
OC Electrophoridae; Electrophorus.
OX NCBI_TaxID=8005;
RN NCBI_TaxID=8005;
RP SEQUENCE FROM N.A.
RX MEDLINE=98070504; PubMed=9407087;
RA Simon S., Massoulié J.;
RT "Cloning and expression of acetylcholinesterase from Electrophorus.
RT Splicing pattern of the 3' exons in vivo and in transfected mammalian
RT cells."
RL J. Biol. Chem. 272:33045-33055(1997).
CC -1- FUNCTION: Rapidly hydrolyzes choline released into the synapse.
CC -1- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF030422; AAB86606.1; -.
CC HSSP; P04058; I123.
DR InterPro: IPR002018; Carboxylesterase.
DR InterPro: IPR000997; Cholinesterase.
DR InterPro: IPR000379; Ser. esters.
DR Pfam; PF00135; Coesterase; 1.
DR PRINTS; PR00878; CHOLINESTRASE.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KM Glycoprotein; Hydrolase; Membrane; Neurotransmitter degradation;
KW Serine esterase; Signal; Synapse.
FT SIGNAL 1 23 Potential.
FT CHAIN 24 633 Acetylcholinesterase.

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FT ACT_SITE 225 225 Acyl-ester intermediate (By similarity).
FT ACT_SITE 352 352 Charge relay system (By similarity).
FT ACT_SITE 494 494 Charge relay system (By similarity).
FT DISULFID 91 118 By similarity.
FT DISULFID 279 290 By similarity.
FT DISULFID 427 579 By similarity.
FT DISULFID 630 630 Interchain (By similarity).
FT CARBOHYD 133 133 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 184 184 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 283 283 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 368 368 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 511 511 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 591 591 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 633 AA; 71814 MW; FC92FE7E4ADB84C3 CRC64;

Query Match 54.5%; Score 1777; DB 1; Length 633;
Best Local Similarity 52.4%; Pred. No. 4,8e-125;
Matches 328; Conservative 108; Mismatches 150; Indels 40; Gaps 7;

Qy 12 PLFWFLLCMLIGKSHTEDDIIATKNGKVRGMILTYFGGT-VTAFGLIPIYAPPLGRIR 70
Db 13 FIMFPIHLISI---AQTPDELLIMTRLGQVQGTPLPVDRSHVIAFLGIPRAEPLGMR 68
Qy 71 FKKPQSLTKASDINWATKANSCCNIDQSPFGHSGEMNPNITDLSBCLYLVWVIPA- 129
Db 69 FKPEPKKPMNDVFPARYPKACYQYVDTSTYPSGSGTMMKPNRMSBDCLYLVWVIPA- 128
Qy 130 PKPKNATVLIWYGGGFGTGTSSLHVYDGKFLARVRYVVMYRVGALFLALPGNPE 189
Db 129 PRPHNLTWVWYGGGFGTGTSSLHVYDGKFLARVRYVVMYRVGALFLALPGNPE 188
Qy 190 APGNMGLFDQRLALQWQENTASFGCNPKSVTLPEESGAASVSHILSPKSHPLFR 249
Db 189 APGNMGLFDQRLALQWQENTASFGCNPKSVTLPEESGAASVSHILSPKSHPLFR 248
Qy 250 LOSGSMNAPWATSLYEARNRTNLAKLTCGSRNETEIIKCLRNKQPOBILNEAFV 309
Db 249 LOSGSMNAPWATSLYEARNRTNLAKLTCGSRNETEIIKCLRNKQPOBILNEAFV 308
Qy 249 LOSGVNGEMRWTVSFDENARRAIKGLVGCDDNDTDLICLRKQODLIDQEMVLIP 308
Db 310 YGTPPLSVNPGFTVDGFLTMDPDLILBGOFRKQIILVGNVKDQSGMTLVYAGAPFKSKDN 369
Db 309 FSGLFPSFVPYIDGVVPDTPDEAMLSGNFQOTQILGVNONESYFLIYAGAPFKSKDN 368
Qy 370 NSIITRKEPOBGLKIFPGVSEFGKESILFHTYDWDVDDQRPENYREALGVVGYNFI 429
Db 369 ESDITREDPLQGVKMSVPMANETGLEAVILQYTDWENQKPEHRDAMDVIGDYHVC 428
Qy 430 ALBFTKKFSR-----MGN-----NAFFYFEHRSKSLPME 460
Db 429 LQHPAKMYAOYSLLOGOTGTAGSGNKGWNSGASNSGVSYLIMYMDHRASNLVWPE 488
Qy 461 WGVMEGYEIEFVFGIPLERRDNTYAEELLSRYKRAMNPAKYNPNETQNNST 517
Db 489 WGVMEGYEIEFVFGIPLERRDNTYAEELLSRYKRAMNPAKYNPNETQNNST 516
Qy 518 -WPFKSTEOXYLTINTESTRIMTKLRAQOCRPWTSFPFKVLEMTGNIDAEEMWAGF 576
Db 549 RWPFPSTEOXYLTINTESTRIMTKLRAQOCRPWTSFPFKVLEMTGNIDAEEMWAGF 608
Qy 577 RNNVYMDMKNQFNDYTSKKSQCVGL 602
Db 609 RNNVYMDMKNQFNDYTSKKSQCVGL 602
RESULT 12
ACES_BRARE STANDARD; PRT; 634 AA.
ID ACES_BRARE STANDARD; PRT; 634 AA.
AC 09DD63:
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Acetylcholinesterase precursor (EC 3.1.1.7) (AChE).
KW Serine esterase; Signal; Synapse.
FT SIGNAL 1 23 Potential.
FT CHAIN 24 633 Acetylcholinesterase.

```

OS Brachydanio rerio (Zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 NCBI\_TaxId=7955;  
 RN [1]  
 RX MEDLINE=20576389; PubMed=11016933; DOI=10.1074/jbc.M006308200;  
 RA Bertrand C., Chastouet A., Takke C., Yan Y., Postlethwait J.,  
 RA Toulant J.-P., Cousin X.;  
 RT "Zebrafish acetylcholinesterase is encoded by a single gene localized  
 on linkage group 7. gene structure and polymorphism; molecular forms  
 and expression pattern during development";  
 RL J. Biol. Chem. 276:464-474(2001).  
 CC -1- FUNCTION: Rapidly hydrolyzes choline released into the synapse.  
 CC -1- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.  
 CC -1- SUBUNIT: Dimers and collagen-tailed forms, in which catalytic  
 tetramers are associated with anchoring proteins that attach them  
 to the basal lamina or to cell membranes. In the collagen-tailed  
 forms, subunits are associated with a specific collagen, COLQ,  
 which triggers the formation of isoform T tetramers from dimers.  
 CC -1- MISCELLANEOUS: No other isoforms exist. This protein corresponds  
 to the T isoform in other species.  
 CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.  
 CC -----  
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 CC -----  
 DR EMBL: AJ251640; CAC19790.1; -  
 DR HSCP; P04058; I123.  
 DR ZFIN: ZDB-GENE-010906-1; ache.  
 DR InterPro: IPR002018; Carboxylesterase.  
 DR InterPro: IPR000997; Cholinesterase.  
 DR InterPro: IPR000379; Ser esterase.  
 DR Pfam: PF00135; Coesterase; 1.  
 DR PRINTS: PR00878; CHOLINESTERASE.  
 DR PROSITE: PS00122; CARBOXYLESTERASE\_B\_1; 1.  
 DR GLYCOPTREIN: Hydroxylase; Membrane; Neurotransmitter degradation;  
 KM Serine esterase; Signal; Synapse.  
 KW SIGNAL  
 FT CHAIN 1 23 Potential.  
 FT ACT\_SITE 225 634 Acetylcholinesterase.  
 FT ACT\_SITE 352 352 Acyl-ester intermediate (By similarity).  
 FT ACT\_SITE 495 495 Charge relay system (By similarity).  
 FT DISULFID 91 118 Charge relay system (By similarity).  
 FT DISULFID 279 290 By similarity.  
 FT DISULFID 427 580 By similarity.  
 FT DISULFID 631 631 Interchain (By similarity).  
 FT CARBOHYD 133 133 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 184 184 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 283 283 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 368 368 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 512 512 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 592 592 N-linked (GlcNAc...) (Potential).  
 SQ SEQUENCE 634 AA; 71998 MW; 47F348E8A7C1B52 CRC64;  
 Query Match 54.2%; Score 1766.5; DB 1; Length 634;  
 Best Local Similarity 52.7%; Pred. No. 3e-124;  
 Matches 323; Conservative 107; Mismatches 146; Indels 37; Gaps 6;

QY 144 GGFOTGTSLSHYVYDGKELAREVETVSNMYRVAGLGLFLLPQNPAPAGNMGJEDQQLAT 203  
 DB 143 GGFYSGSSSLDYVDGRLATATEKVVSVMYRVAGLFGFLALNSSDAPGVNGLYDQQLAT 202  
 QY 204 QWVQKNTAARFGNPKPSTTLFGESAGASVSLHLSPOSHSLFTRAILIQSSFPNPAVTS 263  
 DB 203 QWVQENHFFGPGPKQVTLTIGESAGASVGMHVLSPDSRPLFTRAILIQSSVPMPTAVTS 262  
 QY 264 LYEARNNTLALKLTGSRNENETIICKLNKPOEILNLEAFVVPYGTPLSNVFGPTVD 323  
 DB 263 FDEARRRTTKLGLVGTGWDNTELDCLNKNKPIDELIDQEWYLPWSSLPFRSFVVD 322  
 QY 324 GDPFLTPMDLILELQGFCKTQIIVGVNKEDEGTFLVYGAFPSKDNNSITTRKEPQGLK 383  
 DB 323 GVFPFDPDAMISGNKQYQILLGVVQDEGSFLLYGAFSGKDNSSLRSRDFLESVK 382  
 QY 384 IFFPGVSEPKESILFHYTDVDDQRPENYREALGDVGYNYFCPALBETKPFSE--- 439  
 DB 383 MGVPHANDIGLEAVIILQYTDMDENNQKRDAMDIDVGDQNYICPLQHPAKSYAQYAL 442  
 QY 440 -----WGN-----AFYYPEHRSKLPWPEMGMVHGTEIEFV 473  
 DB 443 HAQSSAAPPTLQWNSGPTGNSGNSHGAIVYLFDHRASNLAMPKMGVHGYETEFV 502  
 QY 474 FGLPLERRDNYTAAEILSRISIVRWANFAKYGNP-----ETQNNSTMPVPFKSTQKYL 529  
 DB 503 FGLPLEKRLNYTAAEELSLRIRMYANFARTGNPNVNTGDSRRRWQFSANDEKXV 562  
 QY 530 TLNTESTRLMTKLPAQCRFTWSPFPKYLEMTGNIDEAEWEKAGFRRNNYMDWKQF 589  
 DB 563 GLNTEPMKVKHGKRTQFCALMNRFLPRLNITNDIVERQMKVEFHRMSYMMGHWSQF 622  
 QY 590 NDTYSKKEGCVGL 602  
 DB 623 DHY-SKQERCTDL 634  
 RESULT 13  
 ACES\_BUNFA STANDARD; PRT; 606 AA.  
 ID ACES\_BUNFA  
 AC Q92035; Q73748; Q10720;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 10-OCT-2003 (Rel. 42, Last sequence update)  
 DT 01-OCT-2004 (Rel. 45, Last annotation update)  
 DE Acetylcholinesterase precursor (EC 3.1.1.7) (Ache).  
 OS Bungarus fasciatus (Banded Krait).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Scleroglossae; Serpentes; Colubroidea;  
 OC Elapidae; Bungarinae; Bungarus.  
 NCBI\_TaxId=6613;  
 RN [1]  
 RX SEQUENCE FROM N.A. (ISOFORM S).  
 RC TISSUE=Venom gland;  
 RX MEDLINE=96279007; PubMed=8662867;  
 RA Cousin X., Bon S., Duval N., Maessoulie J., Bon C.;  
 RT "Cloning and expression of acetylcholinesterase from Bungarus  
 fasciatus venom. A new type of COOH-terminal domain; involvement of a  
 positively charged residue in the peripheral site.";  
 RL J. Biol. Chem. 271:15099-15108(1996).  
 RN [2]  
 RX SEQUENCE OF 512-606 FROM N.A. (ISOFORM S AND T), SUBUNIT, AND TISSUE  
 RP SPECIFICITY.  
 RC TISSUE=Liver, and Muscle;  
 RX MEDLINE=98212017; PubMed=9545320;  
 RA Cousin X., Bon S., Maessoulie J., Bon C.;  
 RT "Identification of a novel type of alternatively spliced exon from the  
 acetylcholinesterase gene of Bungarus fasciatus. Molecular forms of  
 acetylcholinesterase in the snake liver and muscle.";  
 RL J. Biol. Chem. 273:9812-9820(1998).  
 RN [3]  
 RX SEQUENCE OF 206-220; 253-272; 321-340; 347-372 AND 503-511.  
 RP TISSUE=Venom;

RX MEDLINE=96244524; PubMed=8674549;  
 RA Cousin X., Crennon C., Grassi J., Meflah K., Cornu G., Sallou B.,  
 RA Bon S., Massoulié J., Bon C.;  
 RT "Acetylcholinesterase from Bungarus venom: a monomeric species";  
 RL FEBS Lett. 387:196-200(1996).  
 CC -1- FUNCTION: Rapidly hydrolyzes choline released into the synapse.  
 CC -1- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.  
 CC -1- SUBUNIT: Isoform S is monomeric. Isoform T can form oligomers,  
 CC including collagen-tailed forms.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=T;  
 CC IsoId=Q92035-2; Sequence=Displayed;  
 CC Name=S;  
 CC IsoId=Q92035-1; Sequence=VSP 008215;  
 CC -1- TISSUE SPECIFICITY: Liver and muscle contain both isoform T and  
 CC isoform S. Venom gland predominantly contains isoform S.  
 CC -1- PTM: The N-terminus is blocked.  
 CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.  
 CC -1- CAUTION: It is uncertain whether Met-1 or Met-9 is the initiator.  
 CC  
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 CC  
 CC EMBL, U54591; AAC59905.1; -;  
 CC EMBL, AF045238; AAC16420.1; -;  
 CC EMBL, AF045238; AAC16421.1; -;  
 CC HSP: P04058; 1H23.  
 CC InterPro: IPR002018; Carboxylesterase.  
 CC InterPro: IPR000997; Cholinesterase.  
 CC InterPro: IPR000998; Fish\_Ache.  
 CC InterPro: IPR000379; Ser\_estrs.  
 CC Pfam: PF00135; Coesterase; 1.  
 CC PRINTS: PR00878; CHOLINESTRASE.  
 CC DR PROSITE: PS00122; CARBOXYLESTERASE B 1; 1.  
 CC DR PROSITE: PS00941; CARBOXYLESTERASE B 2; 1.  
 CC KW Alternative splicing; Direct protein degradation; Glycoprotein;  
 KW Hydrolyase; Membrane; Neurotransmitter degradation; Serine esterase;  
 KW Signal; Synapse.  
 KW  
 FT SIGNAL 1 28  
 FT CHAIN 29 606  
 FT ACT\_SITE 231 231  
 FT ACT\_SITE 358 358  
 FT ACT\_SITE 471 471  
 FT DISULFID 98 125  
 FT DISULFID 285 296  
 FT DISULFID 433 552  
 FT DISULFID 603 603  
 FT  
 FT CARBOHYD 289 289  
 FT CARBOHYD 374 374  
 FT CARBOHYD 484 484  
 FT CARBOHYD 564 564  
 FT VARSPLIC 567 606  
 FT  
 FT MUTAGEN 101 101  
 FT  
 FT MUTAGEN 316 316  
 FT  
 FT CONFLICT 268 268  
 FT CONFLICT 350 350  
 FT SEQUENCE 606 AA; 68074 MM; B95988AEEA0E5709 CRC64;  
 SQ  
 Query Match 53.1%; Score 1730.5; DB 1; Length 606;  
 Best Local Similarity 51.9%; Pred. No. 1.56-121; Indels 11; Gaps 4;  
 Matches 308; Conservative 114; Mismatches 160;

QY 14 FWF-LILC-----MLIGKSHTEDDIIATKNGKRGMLTVGGTVTAFLGIPYAQPL 66  
 Db 15 WMLDGLCLIPSCVAALBGR--GELKVSQTQSVAGSLPVLGDVSAFLGIPFAPBPL 71  
 QY 67 GRLEFKKPSQILTKMSDITMAATKYANSCCQNIQSPQFHSSEMMNPNTLSECLYINW 126  
 Db 72 GRMFLEKPEPKPQHHLATLSYKPCYQVVDVDSPEFQTEWMNPNRGSSEDCLYINW 131  
 QY 127 IPAPKKNATVLTWYGGGFGTQSSSLAVYDGFPLARVEVIVVSMNRYGALGFLALPG 186  
 Db 132 VPSPEPKDAPLVWYGGGFGSAGSLVDYDGRFLTYTQVILVLSYRGAAGFLGLRG 191  
 QY 187 NPEAPGNNGLPDQALQWQKNAIAFGCNPKSVTLTFGESAGAASVSLHLSFGSHSLFT 246  
 Db 192 SPEAPGNGLDQKLLQWITQNNHPFGGNPRATVTFGESAGAASVGMHLSTQSRFLFQ 251  
 QY 247 RALIQSGSPNAPWATVSLYEARNFTLNLAKLTGCSRENEFEIKCLANKPOEILNEAF 306  
 Db 252 RALIQSGSPNAPWATVTPAESRGRALLGKQLGCHFNNDSELVSCLSKMPQELIDEMS 311  
 QY 307 VVPYGTPLSNVNGPVPVDDPFLTMDPDLLELGGFKQTQIIVGVNKGDTGTFVLYGABGS 366  
 Db 312 VLPYKSIIRFPVPVFDSDFPDTPPEAMLSGNKFKQVLLGVKDGSGYFLIYGLGFGS 371  
 QY 367 KNNNSIITRKEFEQELKIFPGVSEFKESILFHYTWDDQRENTREALGVYGYDNF 426  
 Db 372 KNESELISADPLDEGVRSVPHANDIATDAVLQYTQDQDNEKREALDDIVGHNV 431  
 QY 427 ICPALBFTKSESGMGNNAFFYFHRSSKLPMEPMGMHGELEBPVGLPLERDVYTK 486  
 Db 432 ICPVQFANDYAKRSKYAALFDRASNLMPPMGVPBGHELEFPVGLPLANDSLVTP 491  
 QY 487 AEEILSRSLVKRWANFAYKGNFNETQNNSTSPVFKSTEQKYLTLNTESTRIMTKLRAQ 546  
 Db 492 QEKELSRMRKRYANFARTGNPTDPADSGAMPYTAQPOGVQVLTQPLATOPSLRAOI 551  
 QY 547 CREFTSFPFKVLEMTGNIDEAEWEKAGFHRNNYTMQMKNQOFNYTSKXESC 599  
 Db 552 CAPWNFHFLPLNATDINIEAEKWLBEPLHMSAYMMWKSQFDHY-NKQDRC 603  
 RESULT 14  
 ACES\_HUMAN STANDARD; PRT; 614 AA.  
 ID ACES\_HUMAN  
 AC P22303; Q16169; Q9BXPF7;  
 DT 01-AUG-1991 (Rel. 19, Created)  
 DT 01-AUG-1991 (Rel. 19, Last sequence update)  
 DT 01-OCT-2004 (Rel. 45, Last annotation update)  
 DE Acetylcholinesterase precursor (EC 3.1.1.7) (ACHE).  
 GN Name=ACHE;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9108577; PubMed=2263619;  
 RA Soreq H., Ben-Avitz R., Prody C.A., Seidman S., Gnatt A., Neville L.,  
 RA Lieman-Hurwitz J., Lev-Lehman E., Ginzberg D., Lipidot-Litson Y.,  
 RA Zakut H.;  
 RT "Molecular cloning and construction of the coding region for human  
 RT acetylcholinesterase reveals a G + C-rich attenuating structure";  
 RT Proc. Natl. Acad. Sci. U.S.A. 87:9688-9692(1990).  
 RN [2]  
 RP SEQUENCE OF 521-614 FROM N.A.  
 RX MEDLINE=21138439; PubMed=11239002;  
 RA Wilson M.D., Riemer C., Martindale D.W., Schnupf P., Boright A.P.,  
 RA Cheung T.L., Hardy D.W., Schwartz S., Scherer S.W., Tsui L.-C.,  
 RA Miller W., Koop B.F.;  
 RT "Comparative analysis of the gene-dense ACHE/TFR2 region on human  
 RT chromosome 7q22 with the orthologous region on mouse chromosome 5";  
 RL Nucleic Acids Res. 29:1352-1365(2001).

RP PARTIAL SEQUENCE FROM N.A. (ISOFORM 2).  
 RX MEDLINE=94131004; Pubmed=2299723;  
 RA Karpel R., Ben Azi-Aluya R., Sternfeld M., Ehrlich G., Ginsberg D.,  
 RA Tardov P., Clementi F., Zakut H., Soreq H.,  
 RT "Expression of three alternative acetylcholinesterase messenger RNAs  
 RT in human tumor cell lines of different tissue origins."  
 RL Exp. Cell Res. 210:268-277(1994).  
 RN [4]  
 RP PARTIAL SEQUENCE.  
 RP TISSUE=Erythrocyte;  
 RX MEDLINE=89232135; Pubmed=2714437;  
 RA Chhajiani V., Derr D., Earles B., Schnell E., August T.,  
 RT "Purification and partial amino acid sequence analysis of human  
 RT erythrocyte acetylcholinesterase."  
 RL FEBS Lett. 247:279-282(1989).  
 RN [5]  
 RP MUTAGENESIS OF CYS-611.  
 RX MEDLINE=92084699; Pubmed=1748670;  
 RA Velan B., Grosfeld H., Kromann C., Leitner M., Gozes Y., Lazar A.,  
 RA Flashner Y., Marcus D., Cohen S., Shafferman A.,  
 RT "The effect of elimination of intersubunit disulfide bonds on the  
 RT activity, assembly, and secretion of recombinant human  
 RT acetylcholinesterase. Expression of acetylcholinesterase Cys-580-->Ala  
 RT mutant".  
 RL J. Biol. Chem. 266:23977-23984(1991).  
 RN [6]  
 RP MUTAGENESIS OF ACTIVE SITE RESIDUES AND OF ASP-206 AND ASP-435.  
 RX MEDLINE=92386112; Pubmed=1517212;  
 RA Shafferman A., Kromann C., Flashner Y., Leitner M., Grosfeld H.,  
 RA Orendelich A., Gozes Y., Cohen S., Ariel N., Barak D.,  
 RT "Mutagenesis of human acetylcholinesterase. Identification of residues  
 RT involved in catalytic activity and in polypeptide folding".  
 RL J. Biol. Chem. 267:17640-17648(1992).  
 RN [7]  
 RP 3D-STRUCTURE MODELING OF 35-574.  
 RX MEDLINE=98304745; Pubmed=9640563;  
 RA Felder C.B., Botli S.A., Lifson S., Silman I., Sussman J.L.,  
 RT "External and internal electrostatic potentials of cholinesterase  
 RT models".  
 RL J. Mol. Graph. Model. 15:318-327(1997).  
 RN [8]  
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 36-574.  
 RX MEDLINE=20508217; Pubmed=11053835; DOI=10.1107/S0907444900010659;  
 RA Krysner G., Harel M., Gilek K., Tokor L., Velan B., Lazar A.,  
 RA Kromann C., Barak D., Ariel N., Shafferman A., Silman I.,  
 RA Sussman J.L.,  
 RT "Structures of recombinant native and E202Q mutant human  
 RT acetylcholinesterase complexed with the snake-venom toxin fasciculin-  
 RT II".  
 RL Acta Crystallogr. D 56:1385-1394(2000).  
 RN [9]  
 RP VARIANT BLOOD GROUP Yt(B) ASN-353.  
 RX MEDLINE=93256075; Pubmed=8488842;  
 RA Bartels C.F., Zelinski T., Lockridge O.,  
 RT "Mutation at codon 322 in the human acetylcholinesterase (ACHE) gene  
 RT accounts for Yt blood group polymorphism".  
 RL Am. J. Hum. Genet. 52:928-936(1993).  
 RN [10]  
 RP FUNCTION. Rapidly hydrolyzes choline released into the synapse.  
 CC -1- SUBUNIT: Homodimer; composed of disulfide-linked homodimers.  
 CC -1- INTERACTS WITH PRIMA1: Acetylcholine + H(2)O = choline + acetate.  
 CC -1- INTERACTS WITH PRIMA1: The interaction with PRIMA1 is required to  
 CC anchor it to the basal lamina of cells and organize into tetramers  
 CC (by similarity).  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Comment=Additional isoforms seem to exist;  
 CC Name=1;  
 CC IsoId=P22303-1; Sequence=Displayed;  
 CC Name=2;  
 CC IsoId=P22303-2; Sequence=VSP\_001457;  
 CC -1- POLYMORPHISM: AChE is responsible for the Yt blood group system.  
 CC The molecular basis of the Yt(a)=Yt1/Yt(b)=Yt2 blood group

CC	antigens is a single variation in position 353; His-353	
CC	corresponds to Yt(a) and the rare variant with Asn-353 to Yt(b).	
CC	-1- SIMILARITY: Belongs to the type-B carboxylesterase/1lipase family.	
CC	-1- DATABASE: NME=Blood group antigen mutation database;	
CC	NOTE=Yt blood group system;	
CC	WWW="http://www.bioc.aecom.yu.edu/bgmur/Yt.htm".	
CC	-----	
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CC	or send an email to <a href="mailto:license@idb-eb.ch">license@idb-eb.ch</a> ).	
CC	-----	
DR	EMBL; M55040; AAA68151.1; -	
DR	EMBL; AF312032; AAK21003.1; -	
DR	EMBL; A39256; AAC60618.1; -	
DR	PIR; A39256; A39256; -	
DR	PDB; 1B41; X-ray; A=36-574.	
DR	PDB; 1F8U; X-ray; A=32-614.	
DR	PDB; 2CLJ; Model; @=32-574.	
DR	SWISS-2DPAGE; P22303; HUMAN.	
DR	Gene; HGNC:108; ACHE.	
DR	MIM; 100740; -	
DR	MIM; 112100; -	
DR	GO; GO:0005605; C:basal lamina; NAS.	
DR	GO; GO:0005576; C:extracellular; TAS.	
DR	GO; GO:0042166; F:acetylcholine binding; NAS.	
DR	GO; GO:0003990; F:acetylcholinesterase activity; IMP.	
DR	GO; GO:0001540; F:beta-amyloid binding; TAS.	
DR	GO; GO:0042803; F:protein homodimerization activity; NAS.	
DR	GO; GO:0001507; P:acetylcholine breakdown in synaptic cleft; NAS.	
DR	GO; GO:0042992; P:amyloid precursor protein metabolism; TAS.	
DR	GO; GO:0007155; P:cell adhesion; TAS.	
DR	GO; GO:0008283; P:cell proliferation; TAS.	
DR	GO; GO:0006260; P:DNA replication; TAS.	
DR	GO; GO:0007517; P:muscle development; TAS.	
DR	GO; GO:0050714; P:positive regulation of protein secretion; TAS.	
DR	GO; GO:0009611; P:response to wounding; TAS.	
DR	GO; GO:0007416; P:synaptogenesis; TAS.	
DR	InterPro; IPR002018; CarboxesteraseB.	
DR	InterPro; IPR000997; Cholinesterase.	
DR	InterPro; IPR003179; Ser_estrb.	
DR	Pfam; PF00135; Coesterase; 1.	
DR	PRINTS; PR00878; CHOLNESTRASE.	
DR	PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.	
DR	PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.	
KW	3D-structure; Alternative splicing; Blood group antigen;	
KW	Direct protein sequencing; Glycoprotein; Hydrolase; Membrane;	
KW	Neurotransmitter degradation; Polymorphism; Serine esterase; Signal;	
KW	Synapse.	
FT	SIGNAL	1 31
FT	CHAIN	32 614
FT	ACT_SITE	234 234
FT	ACT_SITE	365 365
FT	ACT_SITE	478 478
FT	DISULFID	100 127
FT	DISULFID	288 288
FT	DISULFID	440 560
FT	DISULFID	611 611
FT	CARBOHYD	296 296
FT	CARBOHYD	381 381
FT	CARBOHYD	495 495
FT	VASSPLIC	575 614
FT	Interchain.	
FT	N-linked (G1CNAC. . .) (Potential).	
FT	N-linked (G1CNAC. . .) (Potential).	
FT	N-linked (G1CNAC. . .) (Potential).	
FT	DTLDEAROKAEFRWSSVWYHKNOFDHYSKDRCSDL	
FT	-> GMQPSASAGRGVGAQCNP8SLPLASAEASTCPGFT	
FT	HGEAAPPFGPLPLLLHQLLLPLSLRRR (in	
FT	isoform 2).	
FT	/FTId=VSP_001457.	
FT	V -> E (in dbSNP:8286).	
FT	/FTId=VAR_011934.	
FT	H -> N (in Yt(b) antigen; dbSNP:1799605).	
FT	/FTId=VAR_002359.	







559 TCFAFNRRFLPKLISATDITDDEARQWKAERHWSSTFWAKNQDFHY-SKQERCSDL 614

RESULT 17

ID	ACCS_MOUSE	STANDARD	PRT	614 AA.
AC	P21836;			
DT	01-MAY-1991 (Rel. 18, Created)			
DT	01-MAY-1991 (Rel. 18, Last sequence update)			
DT	01-OCT-2004 (Rel. 45, Last annotation update)			
DE	Acetylcholinesterase precursor (BC 3.1.1.7) (ACHE).			
OS	Name=ache;			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
NCBI	NCBI_TaxID=10090;			
LN	[1]			
RP	SEQUENCE FROM N.A.			
RP	MDLINE=90380429; PubMed=2400605;			
RA	Rachinsky T.L., Camp S., Li Y., Ekstrom T.J., Newton M., Taylor P.,			
RT	"Molecular cloning of mouse acetylcholinesterase: tissue distribution			
RT	of alternatively spliced mRNA species."			
RL	Neuron 5:317-327(1990).			
LN	[2]			
RP	SEQUENCE FROM N.A.			
RP	STRAIN=129/Sv;			
RC	MDLINE=21138439; PubMed=11239002;			
RA	Wilson M.D., Rimez C., Martindale D.W., Schnupf P., Boright A.P.,			
RA	Cheung T.L., Hardy D.M., Schwartz S., Scherer S.W., Tsai L.-C.,			
RA	Miller W., Koop B.F.;			
RT	"Comparative analysis of the gene-dense ACHE/TR2 region on human			
RT	chromosome 7q22 with the orthologous region on mouse chromosome 5."			
RL	Nucleic Acids Res. 29:1352-1365(2001).			
LN	[3]			
RP	SEQUENCE FROM N.A.			
RP	TISSUE=retina;			
RC	MDLINE=22188577; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strassberg R.L., Felngold E.A., Grouse L.H., Derge J.G., Schuler G.D.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Bhat N.K.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Hsieh F.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,			
RA	Diatchenko L., Marnett K., Farmer A.A., Rubin G.M., Long L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Bromstein M.J., Ubedin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loggellano N.A., Peters K.J., Abramson R.D., Mullaly S.J.,			
RA	Bosak S.A., McSwain P.J., McKernan K.J., Malek J.A., Gumaratre P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Faney J., Helton E., Kettelman M., Medan A.C., Shevchenko Y., Bouffard G.G.,			
RA	Whiting M., Maqan A., Young A.C., Green E.D., Dickson M.C.,			
RA	Blakeley R.W., Touchman J.W., Smith J., Myers R.M.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Smaluk D.E.,			
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smaluk D.E.,			
RA	Schneerch A., Schein J.E., Jones S.J.M., Marra M.A.,			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RT	and mouse cDNA sequences."			
RT	Proc. Natl. Acad. Sci. U.S.A. 99:16699-16903(2002).			
LN	[4]			
RP	INTERACTION WITH PRIMA1.			
RP	MDLINE=21664287; PubMed=11804574;			
RA	Perrier A.L., Massoulie J., Krejci E.;			
RT	"PRIMA1: the membrane anchor of acetylcholinesterase in the brain."			
RL	Neuron 33:275-285(2002).			
LN	[5]			
RP	X-RAY CRYSTALLOGRAPHY (3.2 ANGSTROMS) OF COMPLEX WITH FASCICULIN.			
RP	MDLINE=96067646; PubMed=8521480;			
RA	Bourne Y., Taylor P., Marchot F.;			
RT	"Acetylcholinesterase inhibition by fasciculin: crystal structure of			
RT	the complex."			
RL	Cell 83:503-512(1995).			
LN	[6]			
RP	X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).			

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RX MEDLINE=99115643; PubMed=99158341;
RA Bourne Y, Taylor P., Bougie P.E., Marchot P.;
RT "Crystal structure of mouse acetylcholinesterase. A peripheral site-
RL including loop in a tetrameric assembly.";
RN J. Biol. Chem. 274:2963-2970(1999).
RP [7]
RN RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF 34-573 IN COMPLEX WITH
RP INHIBITOR.
RX PubMed=12505979; DOI=10.1093/emboj/cdg005;
RA Bourne Y., Taylor P., Radic Z., Marchot P.;
RT "Structural insights into ligand interactions at the
RL acetylcholinesterase peripheral anionic site.";
EMBO J. 22:1-12(2003).
CC -1- FUNCTION: Rapidly hydrolyzes choline released into the synapse.
CC -1- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.
CC -1- SUBUNIT: Isoform H generates multiple structures, ranging from
CC linked. Isoform T generates multiple structures, ranging from
CC monomers and dimers to collagen-tailed and hydrophobic-tailed
CC forms, in which catalytic tetramers are associated with anchoring
CC proteins that attach them to the basal lamina or to cell
CC membranes. In the collagen-tailed forms, Isoform T subunits are
CC associated with a specific collagen, COLQ, which triggers the
CC formation of Isoform T tetramers, from monomers and dimers (by
CC similarity). Interacts with PRIMA1. The interaction with PRIMA1 is
CC required to anchor it to the basal lamina of cells and organize
CC into tetramers.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=T;
CC IsoId=P21836-1; Sequence=Displayed;
CC Name=H;
CC IsoId=P21836-2; Sequence=Not described;
CC Note=No experimental confirmation available;
CC -1- TISSUE SPECIFICITY: Predominates in most expressing tissues except
CC erythrocytes where a glycopospholipid-attached form of AChE
CC predominates.
CC -1- MISCELLANEOUS: Synapses usually contain asymmetric molecules of
CC cholinesterase, with a collagen-like part disulfide-bonded to the
CC catalytic part. A different, globular type of cholinesterase
CC occurs on the outer surfaces of cell membranes, including those of
CC erythrocytes.
CC -1- MISCELLANEOUS: This is the catalytic subunit of an asymmetric or
CC soluble form of AChE.
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sdb.cn/announce/
CC or send an email to license@isb-sdb.ch).
CC -----
DR EMBL; X56518; CA39867.1; -
DR EMBL; AF312033; AAK2816.1; -
DR EMBL; BC046323; AAK46327.1; -
DR PIR; JH0314; JH0314.
DR PDB; 1C2B; X-ray; A=35-573.
DR PDB; 1C2O; X-ray; A/B/C/D=36-574.
DR PDB; 1J06; X-ray; A/B=32-574.
DR PDB; 1J07; X-ray; A/B=32-574.
DR PDB; 1K06; X-ray; A=32-580.
DR PDB; 1MAA; X-ray; A/B/C/D=32-578.
DR PDB; 1MAH; X-ray; A=32-574.
DR PDB; 1NSM; X-ray; A/B=32-572.
DR PDB; 1NSR; X-ray; A/B=32-574.
DR PDB; 1O83; X-ray; A/B=1-580.
DR MGD; MGI:87876; Ache.
DR GO; GO:0045202; C:synapse; IDA.
DR InterPro; IPR002018; Carboxylesterase.
DR InterPro; IPR000997; Cholinesterase.
DR InterPro; IPR000379; Ser estse.
DR Pfam; PF00135; Coesterase; 1.

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DR PRINTS; PRO0878; CHOLINESTERASE.  
DR PROSITE; PS00122; CARBOXYLESTERASE\_B\_1; 1.  
DR PROSITE; PS00941; CARBOXYLESTERASE\_B\_2; 1.  
KM 3D-structure; Alternative splicing; Glycoprotein; Hydrolase; Membrane;  
KM Neurotransmitter degradation; Serine esterase; Signal; Synapse.  
FT SIGNAL 1 31  
FT CHAIN 32 614 Acetylcholinesterase.  
FT ACT\_SITE 234 234 Acyl-ester intermediate.  
FT ACT\_SITE 365 365 Charge relay system.  
FT ACT\_SITE 478 478 Charge relay system.  
FT DISULFID 100 127  
FT DISULFID 288 303  
FT DISULFID 440 560  
FT DISULFID 611 611 Interchain (By similarity).  
FT CARBOHYD 296 296 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 381 381 N-linked (GlcNAc...)  
FT CARBOHYD 495 495 N-linked (GlcNAc...)  
FT HELIX 37 39  
FT STRAND 40 43  
FT TURN 44 45  
FT STRAND 46 49  
FT STRAND 51 55  
FT TURN 56 57  
FT STRAND 58 67  
FT STRAND 69 69  
FT HELIX 74 76  
FT TURN 77 78  
FT STRAND 83 83  
FT STRAND 90 92  
FT STRAND 94 94  
FT STRAND 99 100  
FT TURN 109 110  
FT HELIX 112 115  
FT TURN 116 117  
FT STRAND 123 124  
FT STRAND 129 135  
FT STRAND 143 149  
FT TURN 153 155  
FT TURN 159 160  
FT HELIX 162 164  
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FT STRAND 176 180  
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FT STRAND 251 252  
FT STRAND 255 259  
FT STRAND 270 271  
FT HELIX 272 285  
FT TURN 286 287  
FT HELIX 297 304  
FT TURN 305 306  
FT HELIX 309 315

Query Match 51.9%; Score 1692.5; DB 1; Length 614;  
Best Local Similarity 52.1%; Pred. No. 1,le-118;  
Matches 314; Conservative 106; Mismatches 172; Indels 11; Gaps 5;

QY 10 IRLFWLLICMLIGKSHTE---DIIITATKNGKVRGMILTVFGTVTAFLGIPVAQPP 65  
DB 13 IAFPLILLLSLGGGARAEGREDPOLLVVGGQLGIRLKAEGCVSAFLGIPFAEPP 72  
QY 66 LGRIREFKPPQSILTKWSIWNATKXANSCCNIDSPFGFSGEMWNNTDLSEDCLYLVN 125  
DB 73 VGSRRFPPEPKRPMWGVLDATITQNVCYQVDTLVLPFGSTEMWNNRELSDECLYLVN 132

QY 126 WIPAEKPKAT-VLIWYGGGFOTGTSLSHLYVNGKFLARVERIVVSMNRVAGALGFLAL 184  
DB 133 WTPYPRASPTPLIWIYGGGFYSGAASLDVYGRFLAQVEGAVLVSMNRVGFGLAL 192  
QY 185 PGNDPEAPGNNGLPDQOALQWVOKNIAAGGNPKSVTLFPESGAASVSLHLSPGSHL 244  
DB 193 PGSHPEAGNVGLDQRLAQWVOKNIAAGGDDPMSVTLFPESGAASVGMHILSLPERSL 252  
QY 245 FTRAILQSGSFNAPWAVTSLYEARNRTLAKLTGC---SRNETEIIKCLRNKDPQEI 300  
DB 253 FHRNAVLSQGTIPNGPMVAVSAGEARRATLLARLVGCPGAGGNDDELICLTRPAQDL 312  
QY 301 LLINEAFVVPYGTPLSVNGFTVDGFLTMDPILILEGQFKTQILVGNKDGSTWFLVY 360  
DB 313 VDHEMHLVPEESIFRSEFVVDVGDFLSDTPREALINTGDFQDQVLVGVVKGDSGYELVY 372  
QY 361 GAGFGSKDNNSIITRKEFGQGLKIFPGVGEPEKESILFHYTQWVDQRENRREALGDV 420  
DB 373 GVPFGSKDNSSLISRQFLAGVRIQVQASDLAAEAVLHYTMDLHPEDTHLRDMSAV 432  
QY 421 VGDYNFICPALIEFTKFESEWGNNAFFYFPEHRSSKLPMPWMGMVMEGEIEFVGLPLER 480  
DB 433 VGDHNVCPVAQLAGRLAAGARVAYIFHRASLTLMPLMGVPHGYEIEFTFGLPLDP 492  
QY 481 RDNYTKAEITLSRSIVKRWANPAKGNPNETQNN-STSWPEFKSTQKYLTLNTESTRIM 539  
DB 493 SLNYTTEERIFAQRLMKYWTNFPARTGDPNDPDSKSPQMPYTTAAQOYVSLMLKPLEVR 552  
QY 540 TKLRACQCRFWTSFFPPVULEMTGNIDEAEWEMKAGFRMNNVMMDMQNDYTSKKESE 599  
DB 553 RGLRAQTCAPWNPFLPLSLSATDTLDIAERQWRAEFHRSSVYVHWKNDPHY-SKQERC 611  
QY 600 VGL 602  
DB 612 SDL 614

RESULT 18  
BAC31228  
ID BAC31228 PRELIMINARY; PRT; 614 AA.  
AC BAC31228:  
DT 14-APR-2004 (TrEMBLrel. 27, Created)  
DT 14-APR-2004 (TrEMBLrel. 27, Last sequence update)  
DT 14-APR-2004 (TrEMBLrel. 27, Last annotation update)  
DE 3 days neonate thymus cDNA, RIKEN full-length enriched library,  
DE clone: A630083G07 product: acetylcholinesterase, full insert  
DE sequence.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Thymus;  
RC MEDLINE=22354683; PubMed=12466851;  
RA The FANTOM Consortium;  
RA The RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs."  
RL Nature 420:563-573(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Thymus;  
RC MEDLINE=21085660; PubMed=11217851;  
RA RIKEN FANTOM Consortium;  
RA "Functional annotation of a full-length mouse cDNA collection."  
RN Nature 409:685-690(2001).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Thymus;  
RC MEDLINE=99279253; PubMed=10349636;  
RX Carninci P.; Hayashizaki Y.;  
RT "High-efficiency full-length cDNA cloning.";

```

RL Meth. Enzymol. 303:19-44(1999).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
  Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
  prepare full-length cDNA libraries for rapid discovery of new genes."
  Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
  Kono H., Akiyama U., Nishi K., Kitesunai T., Taahiro H., Itoh M.,
  Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
  Yamamoto R., Matsuno H., Sakaguchi S., Ikegami T., Kashiwagi K.,
  Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Wataniki M.,
  Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai U.,
  Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
  sequencing pipeline with 384 multicapillary sequencer."
  Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RA Adachi U., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
  Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
  Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,
  Hori F., Imocani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
  Kato H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
  Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
  Nishi K., Nomura K., Numazaki R., Ono M., Ohnato N., Okazaki Y.,
  Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
  Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
  Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
  Tomaru A., Tota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK042335; BAC1228.1;
SQ SEQUENCE 614 AA; 68168 MW; 66E2512463C21172 CRC64;

Query March 51.9%; Score 1692.5; DB 2; Length 614;
Best Local Similarity 52.1%; Pred. No. 1.1e-118;
Matches 314; Conservative 106; Mismatches 172; Indels 11; Gaps 5;

QY 10 IRLFWFLLCMLIGKSHTE---DDIIATKNGKVRGMNLTFGVTVAFLGIPYQPP 65
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 13 LAFPLLELLSLILGGARAEGRBDPOLIVRVGQGLRIGRLKAPGCVSAFLGIPFAEP 72
QY 66 LGRIRFKKPOSLTKWSDIWNATKXANSCCONIDSPFGHSEKMNNTDSEKCLTVN 125
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 73 VGSRRFPPPEPKRPMGVLATYTONVCYQYVDLTLYPEFBETEMNPRELSEKCLTVN 132
QY 126 WIPAPKPKNAT-VLIWIYGGFGOTGTSIIHYDCKFLARVRYVVMNRYVGAFLAL 184
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 133 WTPYRPASFPFVIMWYIGGFGYGAASLDYDGRFLAQVGVAVLVMNRYVGFGLAL 192
QY 185 PGNDEAPGNMGLFDQOALQWVQKNIAAFGNGPKSVTLFGESAGAAVSLLHSPGSHL 244
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 193 PGSREAPGNVGLDQRLALQWVOENIAAFGCDPMSVTLFGESAGAAVSLLHSPRSL 252
QY 245 PFRALLOGSGFMAWVAVTSLYEANRNTLNAKLQGC-----SRNMTETIKLRKMDQEI 300
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 253 FHRVAVLOSCTPNGPAAVTSAGEARRATLLARLVGCPGAGAGDTEIACLRTPAODL 312
QY 301 LLNEAFVVPYGPPLSVNGPTVDGDFLTMDPDIILEGQFKKTOILVGNODEGTWELVY 360
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 313 VDHEWHTVLPQESIRFSPVVDGDFLSDTEBALINTGDFQDLQVLYVGVVDSBSFLVY 372
QY 361 GAGPSSKNNNSITRKEFOEGIKLFFPGVSEFGKESILFHTYTDVDDQRPENRYBALGV 420
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 373 GVPGSKNNSLISRAQFLAGVIRIGVQASDLAAEAVALHTYDMLHPEDPTRLDDMSAV 432

RESULT 19
BAC1641
ID BAC1641 PRELIMINARY; PRT; 614 AA.
AC BAC1641;
DT 14-APR-2004 (TEMBLrel. 27, Created)
DT 14-APR-2004 (TEMBLrel. 27, Last sequence update)
DE 10 days neonate cortex cDNA, RIKEN full-length enriched library,
DE clone: A030027P05 product: acetylcholinesterase, full insert
DE sequence.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cortex;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium;
RA The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
  60,770 full-length cDNAs."
  Nature 420:563-573(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cortex;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection."
  Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cortex;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning."
  Meth. Enzymol. 303:19-44(1999).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cortex;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
  Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
  prepare full-length cDNA libraries for rapid discovery of new genes."
  Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cortex;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
  Kono H., Akiyama U., Nishi K., Kitesunai T., Taahiro H., Itoh M.,
  Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
  Yamamoto R., Matsuno H., Sakaguchi S., Ikegami T., Kashiwagi K.,
  Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Wataniki M.,

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RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,  
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,  
 RT "RIKEN integrated sequence analysis (RISA) system-384-format  
 RT sequencing pipeline with 384 multicapillary sequencer.",  
 RL Genome Res. 10:1757-1771(2000).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Cortex;  
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
 RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,  
 RA Horii F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
 RA Kato H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,  
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,  
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,  
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,  
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AK043748; BAC31641.1; -  
 SO SEQUENCE 614 AA; 68168 MW; 66E2512463C21172 CRC64;  
 Query Match 51.9%; Score 1692.5; DB 2; Length 614;  
 Best Local Similarity 52.1%; Pred. No. 1,1e-118;  
 Matches 314; Conservative 106; Mismatches 172; Indels 11; Gaps 5;  
 QY 10 IRLFWLLLCMLGKSHTE---DDIIIAKNGKVGMLTVGRTVTAFLGIPYQOP 65  
 DB 13 LAFPLLLSLGCGARBEREDPQLVRGQGLRIGIRKADGPVSAVLGIPFAEP 72  
 QY 66 LGLRFRKPKPOSITATMSDINWATKYANSCQNIIDSPFGFSGEMNPNPTDISECLVNV 125  
 DB 73 VGSRRFPKPKRMSVGLDITTFQNYCYQVDTLYGFEBETEMNPNRREISCLVNV 132  
 QY 126 WIPAPKRNAT-VLIWYGGGFGTGTSSLHVYDGKFLARVIVVSMNTRVGLAL 184  
 DB 133 WTPYRPASPTPLVLIWYGGFGSAGASLDVYDGRFLAQVGVSMNTRVGFGLAL 192  
 QY 185 PGNPEAGNGLPFOQALWQVQNIAGFGNPKSVTLFGSAGASVSLHSPGSHL 244  
 DB 193 PGSEAGNGLDQRLALWQVQNIAGFGDPMSVTLFGSAGASVSMHLSLPSRL 252  
 QY 245 FTFAILOSFSFNAPWATSLYEARNRTLAKLTGC---SRENETELIKLRKDOEI 300  
 DB 253 FRAVAVLOSCTPNGMWATVSAGARRRATLALVGCPCPGAGNDTELIACTIRPQDL 312  
 QY 301 LNEAFVVPYGTPLSVNFGPTVDGFLTMDLLELGOFKKTOILVGNKDEGFWLVY 360  
 DB 313 VDHEWVLPQESIFRFSFVPVVDGFLSDPFEALINTGDFODLVGVVDEGSYFLVY 372  
 QY 361 GAFPSKDNNSITRKPFQBLKTFPGVSEFGESLFLHTDWDVDOORPNRYEALGDV 420  
 DB 373 GVPEFSKDNSSLRAQFLAGVRIGVQASDLAEAVLHTDMLHEDPFLHLDASAV 432  
 QY 421 VGDVNFICPALFTKKESEWNNAFYFYEHSKSLPMEWGMWGHGEIEFVGLPLER 480  
 DB 433 VGDHNVCPVAQLAGRLAAGARVYATIFERASTLWPLMGVPRGIEIFITGLDLP 492  
 QY 481 RDNYYKAEILSRGIVRMANFATYGNPNETQNN-STSPVFKSTOKYTLTNTSTRIM 539  
 DB 493 SLNVTTERIFAQGLMKVMTFAFGDPNDPDSKSPQWPRYTTAAQYVSLNKPFLVR 552  
 QY 540 TKRAQOCRTWTSFPKYLENTGNIDAEWENKAGFRMNNYMDKQGFNDYSKESK 599  
 DB 553 RGLRAQCAFWRNPLPKLLSATDITLDEARQWKAFFRWSSVYVHWKQDPDY-SKQERC 611  
 QY 600 VGL 602  
 DB 612 SDL 614

BAC32595  
 ID BAC32595 PRELIMINARY; PRT; 614 AA.  
 AC BAC32595;  
 DT 14-APR-2004 (TREMBlrel. 27, Created)  
 DT 14-APR-2004 (TREMBlrel. 27, Last sequence update)  
 DT 14-APR-2004 (TREMBlrel. 27, Last annotation update)  
 DE Adult male corpora quadrigemina cDNA, RIKEN full-length enriched  
 DE library, clone:B230340L13 product:acetylcholinesterase, full insert  
 DE sequence.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;  
 RX MEDLINE=22354683; PubMed=12466851;  
 RA The FANTOM Consortium;  
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs";  
 RL Nature 420:563-573(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;  
 RX MEDLINE=21085660; PubMed=11217851;  
 RA RIKEN FANTOM Consortium;  
 RT "Functional annotation of a full-length mouse cDNA collection";  
 RL Nature 409:685-690(2001).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;  
 RX MEDLINE=99279253; PubMed=10349636;  
 RA Carninci P., Hayashizaki Y.,  
 RT "High-efficiency full-length cDNA cloning";  
 RL Meth. Enzymol. 303:19-44(1999).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;  
 RX MEDLINE=20499374; PubMed=11042159;  
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.,  
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
 RT prepare full-length cDNA libraries for rapid discovery of new genes";  
 RL Genome Res. 10:1617-1630(2000).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;  
 RX MEDLINE=20530913; PubMed=11076861;  
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
 RA Kono H., Akimura T., Nishi K., Katsunai T., Taahiro H., Itoh M.,  
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
 RA Yamamoto K., Matsunoto H., Sakaguchi S., Ikegami T., Kasaiwaagi K.,  
 RA Fujikawa R., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,  
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsumura S., Kawai J.,  
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,  
 RT "RIKEN integrated sequence analysis (RISA) system-384-format  
 RT sequencing pipeline with 384 multicapillary sequencer";  
 RL Genome Res. 10:1757-1771(2000).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;  
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
 RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,  
 RA Horii F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
 RA Kato H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,  
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,  
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,  
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,  
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,

RESULT 20







RA Taylor S.S., Taylor P.;  
 RT "Divergence in primary structure between the molecular forms of  
 RT acetylcholinesterase.";  
 RL J. Biol. Chem. 263:1140-1145(1988).  
 RN [6]  
 RP ALTERNATIVE SPLICING.  
 RX MEDLINE=90166618; PubMed=2306366;  
 RA Malet Y., Camp S., Gibney G., Rachinsky T.L., Ekstrom T.J.,  
 RA Taylor P.;  
 RT "Single gene encodes glycopospholipid-anchored and asymmetric  
 RT acetylcholinesterase forms: alternative coding exons contain inverted  
 RT repeat sequences.";  
 RL Neuron 4:289-301(1990).  
 RN [7]  
 RP DISULFIDE BONDS.  
 RX MEDLINE=87008586; PubMed=3759980;  
 RA McPhee-Quigley K., Vetric T.S., Taylor P., Taylor S.S.;  
 RT "Profile of the disulfide bonds in acetylcholinesterase.";  
 RL J. Biol. Chem. 261:13565-13570(1986).  
 RN [8]  
 RP STRUCTURE OF THE GPI-ANCHOR.  
 RX MEDLINE=94079692; PubMed=8257440;  
 RA Mehler A., Varon L., Silman I., Homans S.W., Ferguson M.A.;  
 RT "Structure of the glycosyl-phosphatidylinositol membrane anchor of  
 RT acetylcholinesterase from the electric organ of the electric fish,  
 RT Torpedo californica.";  
 RL Biochem. J. 296:473-479(1993).  
 RN [9]  
 RP GPI-ANCHOR.  
 RX MEDLINE=96176849; PubMed=8597567; DOI=10.1016/0167-4838(95)00205-7;  
 RA Bucht G., Hjalmarsson K.;  
 RT "Residues in Torpedo californica acetylcholinesterase necessary for  
 RT processing to a glycosyl phosphatidylinositol-anchored form.";  
 RL Biochim. Biophys. Acta 1252:223-232(1996).  
 RN [10]  
 RP MOTAGENESIS.  
 RX MEDLINE=91017542; PubMed=2217185;  
 RA Gibney G., Camp S., Dionne M., McPhee-Quigley K., Taylor P.;  
 RT "Mutagenesis of essential functional residues in  
 RT acetylcholinesterase.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 87:7546-7550(1990).  
 RN [11]  
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).  
 RX MEDLINE=91343928; PubMed=1678899;  
 RA Sussman J.L., Harel M., Frolow F., Oefner C., Goldman A., Tokar L.,  
 RA Silman I.;  
 RT "Atomic structure of acetylcholinesterase from Torpedo californica: a  
 RT prototypic acetylcholine-binding protein.";  
 RL Science 253:872-879(1991).  
 RN [12]  
 RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS) OF COMPLEX WITH FASCICULIN.  
 RX MEDLINE=96366673; PubMed=8747462;  
 RA Harel M., Kleweg G.J., Raveill R.B., Silman I., Sussman J.L.;  
 RT "Crystal structure of an acetylcholinesterase-fasciculin complex:  
 RT interaction of a three-fingered toxin from snake venom with its  
 RT target.";  
 RL Structure 3:1355-1366(1995).  
 RN [13]  
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).  
 RX MEDLINE=97143314; PubMed=8989325;  
 RA Raves M.L., Harel M., Pang Y.P., Silman I., Kozikowski A.P.,  
 RA Sussman J.L.;  
 RT "Structure of acetylcholinesterase complexed with the nootropic  
 RT alkaloid, (-)-huperzine A.";  
 RL Nat. Struct. Biol. 4:57-63(1997).  
 RN [14]  
 RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).  
 RX MEDLINE=99249780; PubMed=10231521;  
 RA Bartolucci C., Perola E., Cellai L., Brufani M., Lamba D.;  
 RT "Back door" opening implied by the crystal structure of a  
 RT carbamoylated acetylcholinesterase.";  
 RL Biochemistry 38:5714-5719(1999).  
 RN [15]

RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).  
 RX MEDLINE=99282167; PubMed=10353814;  
 RA Millard C.B., Kryger G., Ordentlich A., Greenblatt H.M., Harel M.,  
 RA Raves M.L., Segall Y., Barak D., Shafferman A., Silman I.,  
 RA Sussman J.L.;  
 RT "Crystal structures of aged phosphorylated acetylcholinesterase: nerve  
 RT agent reaction products at the atomic level.";  
 RL Biochemistry 38:7032-7039(1999).  
 RN [16]  
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).  
 RX MEDLINE=20074924; PubMed=10606746;  
 RA Greenblatt H.M., Kryger G., Lewis T., Silman I., Sussman J.L.;  
 RT "Structure of acetylcholinesterase complexed with (-)-galanthamine at  
 RT 2.3-A resolution.";  
 RL FEBS Lett. 463:321-326(1999).  
 RN [17]  
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).  
 RX MEDLINE=99197295; PubMed=10368299;  
 RA Kryger G., Silman I., Sussman J.L.;  
 RT "Structure of acetylcholinesterase complexed with E2020 (Aricept(R)):  
 RT implications for the design of new anti-alzheimer drugs.";  
 RL Structure 7:397-307(1999)  
 CC -1- FUNCTION: Rapidly hydrolyzes choline released into the synapse.  
 CC May be involved in cell-cell interactions.  
 CC -1- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.  
 CC -1- SUBUNIT: The H form is an homodimer; the asymmetric form is a  
 CC disulfide-bonded oligomer composed of a collagenic subunit (Q) and  
 CC a variable number of T catalytic subunits.  
 CC -1- SUBCELLULAR LOCATION: The H form is attached to the membrane by a  
 CC GPI-anchor.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Comment=Additional isoforms seem to exist;  
 CC Name=H; Synonyms=Globular;  
 CC IsoId=P04058-1; Sequence=displayed;  
 CC Name=T;  
 CC IsoId=P04058-2; Sequence=VSP\_001460;  
 CC -1- TISSUE SPECIFICITY: Found in the synapses and to a lower extent in  
 CC extrajunctional areas of muscle and nerve, and on erythrocyte  
 CC membranes.  
 CC -1- PTM: An interchain disulfide bond is present in what becomes  
 CC position 593 of the T isoform.  
 CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 CC EMBL: X03439; CAA27169.1; -;  
 CC EMBL: X56516; -; NOT\_ANNOTATED\_CDS.  
 CC EMBL: X56517; -; NOT\_ANNOTATED\_CDS.  
 CC PIR: A00773; ACRYE.  
 CC PDB: 1ACU; X-ray; @=22-558.  
 CC PDB: 1AMN; X-ray; @=22-558.  
 CC PDB: 1AX9; X-ray; @=22-558.  
 CC PDB: 1CFJ; X-ray; A=22-558.  
 CC PDB: 1DX6; X-ray; A=22-564.  
 CC PDB: 1E3Q; X-ray; A=22-564.  
 CC PDB: 1E66; X-ray; A=22-564.  
 CC PDB: 1EA5; X-ray; A=22-558.  
 CC PDB: 1EVA; X-ray; A=22-555.  
 CC PDB: 1FSS; X-ray; @=22-564.  
 CC PDB: 1GPN; X-ray; A=22-558.  
 CC PDB: 1GPR; X-ray; A=22-558.  
 CC PDB: 1GQR; X-ray; A=25-556.  
 CC PDB: 1GQS; X-ray; A=25-556.  
 CC PDB: 1H22; X-ray; A=22-564.







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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 6, 2005, 09:28:32 ; Search time 43 Seconds  
(without alignments)  
1347.035 Million cell updates/sec

Title: us-09-748-739a-2

Perfect score: 3260  
Sequence: 1 MDSKVITICIRFLFWILLC.....MDMKQFNQDYTSKKECVGL 602

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 100 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3239	99.4	602	1	CHOLINESTERASE (EC
2	2855.5	87.6	581	2	CHOLINESTERASE (EC
3	2593	79.5	603	2	CHOLINESTERASE (EC
4	1791.5	55.0	596	1	ACRYL
5	1789.5	54.9	599	1	ACRYL
6	1698.5	52.1	614	2	ACRYL
7	1693.5	51.9	614	2	ACRYL
8	1692.5	51.9	614	2	ACRYL
9	1639	50.2	584	2	ACRYL
10	1636.5	50.2	583	2	ACRYL
11	1466	45.0	767	2	ACRYL
12	1142	35.0	620	2	ACRYL
13	1075.5	33.0	637	2	ACRYL
14	1045	32.1	691	2	ACRYL
15	1044	32.0	746	2	ACRYL
16	1038.5	31.9	664	2	ACRYL
17	1025.5	31.5	602	2	ACRYL
18	951	29.2	629	2	ACRYL
19	937	28.7	584	2	ACRYL
20	930	28.5	607	2	ACRYL
21	893	27.4	532	2	ACRYL
22	754	23.1	532	2	ACRYL
23	753	22.7	141	2	ACRYL
24	740.5	22.5	559	2	ACRYL
25	733	22.4	559	2	ACRYL
26	731.5	22.4	561	2	ACRYL
27	729	22.3	597	2	ACRYL
28	727	22.3	612	2	ACRYL
29	724.5	22.2	554	2	ACRYL

30	724	22.2	141	2	D39768	cholinesterase (EC
31	721	22.1	141	2	F39768	cholinesterase (EC
32	721	22.1	141	2	B39768	cholinesterase (EC
33	716	22.0	565	2	S10367	carboxylesterase (
34	713.5	21.9	562	2	A55281	carboxylesterase (
35	711	21.8	745	2	S13586	triacylglycerol li
36	707	21.7	141	2	E39768	cholinesterase (EC
37	701.5	21.5	557	2	A47162	cholinesterase B (E
38	700.5	21.5	567	2	A41010	carboxylesterase (
39	700	21.5	561	2	JC2447	carboxylesterase (
40	699.5	21.5	549	2	JX0054	carboxylesterase (
41	697	21.4	540	2	A31584	carboxylesterase (
42	692	21.2	561	2	S62788	carboxylesterase (
43	691	21.2	561	2	S71597	carboxylesterase (
44	690.5	21.2	566	2	S19307	carboxylesterase (
45	666	20.4	956	2	A56920	glycactin precurs
46	656.5	20.1	554	1	S34607	carboxylesterase (
47	649	19.9	540	2	S51043	carboxylesterase (
48	636	19.5	2769	1	UIBO	chrysotholubulin prec
49	632.5	19.4	967	1	UIRT	chrysotholubulin - ra
50	627	19.2	540	2	A75250	carboxylesterase (
51	624	19.1	593	1	S25062	triacylglycerol li
52	620	19.0	539	2	A29923	carboxylesterase (
53	604	18.5	2767	1	UIHU	chrysotholubulin prec
54	603.5	18.5	562	2	S27782	esterase precursor
55	599.5	18.4	544	1	S36787	carboxylesterase (
56	594	18.2	489	2	B96880	para-nitrobenzyl e
57	589.5	18.1	583	2	T25690	hypothetical prote
58	587.5	18.0	552	2	S36786	carboxylesterase (
59	585	17.9	506	2	H75522	probable carboxyle
60	585	17.9	554	2	T31783	hypothetical prote
61	585	17.9	557	2	A56690	esterase - Caenorh
62	574.5	17.6	564	2	T28949	hypothetical prote
63	556	17.1	547	2	T29717	hypothetical prote
64	554.5	17.0	562	2	S27800	elastase precursor
65	553	17.0	548	2	T32807	hypothetical prote
66	548.5	16.8	550	1	A34576	crystal protein pr
67	540.5	16.6	730	2	T32061	gut-specific carbo
68	538.5	16.5	730	2	T16455	hypothetical prote
69	534.5	16.4	578	2	F89068	protein T28C12, 4b
70	534.5	16.4	658	2	T32053	hypothetical prote
71	531.5	16.3	502	2	AE0666	probable esterase
72	526	16.1	543	2	T27000	hypothetical prote
73	522.5	16.0	798	2	T19864	hypothetical prote
74	522	16.0	565	2	T29718	protein B0238.1 [i
75	520.5	16.0	545	2	A89046	protein B0238.1 [i
76	520	16.0	535	2	B34576	D2 protein precurs
77	520	16.0	535	2	A35286	esterase B1 - bout
78	512	15.7	540	2	S53371	carboxylesterase (
79	510	15.6	571	2	G89123	protein K07C11.4 [
80	508	15.6	540	2	S53370	carboxylesterase (
81	501.5	15.4	578	2	B89045	protein B0238.7 [i
82	497	15.2	549	2	UN0552	triacylglycerol li
83	491	15.1	453	2	G89045	protein B0238.2 [i
84	490.5	15.0	544	2	A34325	juvenile-hormone e
85	490	15.0	544	2	B40122	carboxylesterase (
86	490	15.0	544	2	A41426	carboxylesterase (
87	490	15.0	544	2	A34089	carboxylesterase (
88	490	15.0	548	2	A28022	carboxylesterase (
89	489	15.0	544	2	C41426	carboxylesterase (
90	488	14.9	544	2	D41426	carboxylesterase (
91	485	14.9	544	2	A41426	carboxylesterase (
92	485	14.9	544	2	A41426	carboxylesterase (
93	484	14.8	544	2	F41426	carboxylesterase (
94	482	14.8	544	2	B41426	carboxylesterase (
95	482	14.8	544	2	S41094	triacylglycerol li
96	481	14.8	544	2	H41426	carboxylesterase (
97	481	14.8	563	1	PN0493	triacylglycerol li
98	479	14.7	544	2	A34095	triacylglycerol li
99	478.5	14.7	544	2	B34089	carboxylesterase (
100	478	14.7	544	2	E41426	carboxylesterase (

## RESULT 1

## ALIGNMENTS

ACHU (1991: 16) discusses [11] as follows:

cholinesterase (EC 3.1.1.8) precursor (Valiadeu) - human

```
N;AlternateNames: acylcarnitine acylglutamate, acyl-L-homoserine  
C;Species: Homo sapiens (man)
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Query Match 87.6%; Score 2855.5; DB 2; Length 581;  
 Best Local Similarity 91.4%; Pred. No. 1.8e-210;  
 Matches 531; Conservative 12; Mismatches 37; Indels 1; Gaps 1;

QY 21 MLIGKSTHEDDIIATKNGKRGKGNLVYFGSTVTAFLGIPAPQPLRLRKQSLTKW 80  
 DB 1 MVRSSHTT-DVITTTNGRIRGINLPVFGGTVAFLGIPAPQPLRLRKQSLTKW 59  
 QY 81 SDIWNATKYANSCCONIDQSPFGHSGEMNPNITLSDCLYLWVWPAPPKNAATLW 140  
 DB 60 SDIWNATKYANSCCONIDQSPFGHSGEMNPNITLSDCLYLWVWPAPPKNAATLW 119  
 QY 141 IYGGFQGTGSSLHYDGKFLARVERVIVSMNRYVGLGFLALPGNPEAPGNGLPQQ 200  
 DB 120 IYGGFQGTGSSLHYDGKFLARVERVIVSMNRYVGLGFLALPGNPEAPGNGLPQQ 179  
 QY 201 LALQWQKNTAAFGNPKSVTLFGESAGASVSHLSPGSHSLFTRAILQSGSPAPWA 260  
 DB 180 LALQWQKNTAAFGNPKSVTLFGESAGASVSHLSPGSHSLFTRAILQSGSSNAPWE 239  
 QY 261 VTSLYEARNRTLNKLTCGSRNMTETIKCLRNKQPOEILNEAFVVPYGTPLSVNPGP 320  
 DB 240 VMSLHERNRTLTAKVGVGSTEENETETIKCLRNKQPOEILNEAFVVPYGTPLSVNPGP 299  
 QY 321 TVDQDFLTMDPDLLELQGFKKTOILVGNKDEGTWFLVYGAPGFSKDNNSITTRKSFQ 380  
 DB 300 TVDQDFLTMDPDLLELQGFKKTOILVGNKDEGTWFLVYGAPGFSKDNNSITTRKSFQ 359  
 QY 381 GLKTFPGVSGFEGESILFHYTDVDDORPENRYEALGDVVDGNFICPALFPTKSEW 440  
 DB 360 GLKTFPGVSGFEGESILFHYTDVDDORPENRYEALGDVVDGNFICPALFPTKSEW 419  
 QY 441 GNNAFYFFFEHRSKSLPMPWGMVGHGEIEFVGLPLERDNTYKAEILSRISIVRWA 500  
 DB 420 GNNAFYFFFEHRSKSLPMPWGMVGHGEIEFVGLPLERDNTYKAEILSRISIVRWA 479  
 QY 501 NFATGYNPNETONNSTMPVEFKSTEOKYTLTNTSESTRIMTKLRAQOQCRFWTSPPKYLEM 560  
 DB 480 NFATGYNPNETONNSTMPVEFKSTEOKYTLTNTSESTRIMTKLRAQOQCRFWTSPPKYLEM 539  
 QY 561 TGNIDAEWEWKAGFHRNNYMMQNDWKQFNDYTSKESCVG 601  
 DB 540 TGNIDAEWEWKAGFHRNNYMMQNDWKQFNDYTSKESCVG 580

RESULT 3

S70849  
 Cholinesterase (EC 3.1.1.8) - mouse  
 N:Alternate names: butyrylcholine esterase  
 C:Species: Mus musculus (house mouse)  
 C:Date: 28-Oct-1996 #sequence revision 08-Nov-1996 #text\_change 09-Jul-2004  
 A:Accession: S70849; S15680; A39768  
 R:Taylor, P.  
 submitted to the EMBL Data Library, August 1992  
 A:Reference number: S70849  
 A:Accession: S70849  
 A:Molecule type: nucleic acid  
 A:Residues: 1-603 <TRY>  
 A:Cross-references: UNIPROT:Q03311; EMBL:M99492; NID:G191579; PIDD:AAA37328.1; PID:G1915  
 R:Schunacher, M.; Camp, S.; Li, Y.; Ekstrom, T.J.; Newton, M.; Taylor, P.  
 A:Title: Molecular cloning of mouse acetylcholinesterase: tissue distribution of alterna  
 A:Reference number: JH0314; MUID:90380423; PMID:2400605  
 A:Accession: S15680  
 A:Status: nucleic acid sequence not shown  
 A:Molecule type: nucleic acid  
 A:Residues: 30-128, 'P', 130-603 <RAC>  
 A:Cross-references: EMBL:M99492  
 R:Arpagaus, M.; Chalmers, A.; Masson, P.; Newton, M.; Vaughan, T.A.; Bartels, C.F.; Noe  
 J. Biol. Chem. 266, 6966-6974, 1991  
 A:Title: Use of the polymerase chain reaction for homology probing of butyrylcholinester  
 A:Reference number: A39768; MUID:91201348; PMID:2016308

A:Accession: A39768  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 97-128, 'P', 130-237 <ARP>  
 C:Superfamily: cholinesterase; cholinesterase homology  
 C:Keywords: carboxylic ester hydrolase; glycoprotein  
 F:57-557/Domain: cholinesterase homology <CH>

Query Match 79.5%; Score 2593; DB 2; Length 603;  
 Best Local Similarity 80.4%; Pred. No. 2.4e-190;  
 Matches 475; Conservative 47; Mismatches 69; Indels 0; Gaps 0;

QY 12 PLFWFLICMLIGKSTHEDDIIATKNGKRGKGNLVYFGSTVTAFLGIPAPQPLRLR 71  
 DB 13 PLFWFLICMLIGKSTHEDDIIATKNGKRGKGNLVYFGSTVTAFLGIPAPQPLRLR 72  
 QY 72 KKQOSLTMSDINATKYANSCCONIDQSPFGHSGEMNPNITLSDCLYLWVWPAPK 131  
 DB 73 KKQOSLTMSDINATKYANSCCONIDQSPFGHSGEMNPNITLSDCLYLWVWPAPK 132  
 QY 132 PKNATVLIWYGGFQGTGSSLHYDGKFLARVERVIVSMNRYVGLGFLALPGNPEAP 191  
 DB 133 PKNATVLIWYGGFQGTGSSLHYDGKFLARVERVIVSMNRYVGLGFLALPGNPEAP 192  
 QY 192 GNNGLFDQALQWQKNTAAFGNPKSVTLFGESAGASVSHLSPGSHSLFTRAILQ 251  
 DB 193 GNNGLFDQALQWQKNTAAFGNPKSVTLFGESAGASVSHLSPGSHSLFTRAILQ 252  
 QY 252 SGSPNAPWATSLYEARNRTLNKLTCGSRNMTETIKCLRNKQPOEILNEAFVVPY 311  
 DB 253 SGSPNAPWATSLYEARNRTLNKLTCGSRNMTETIKCLRNKQPOEILNEAFVVPY 312  
 QY 312 TPISVNFPTVDGFLTMDPDLLELQGFKKTOILVGNKDEGTWFLVYGAPGFSKDNNS 371  
 DB 313 TPISVNFPTVDGFLTMDPDLLELQGFKKTOILVGNKDEGTWFLVYGAPGFSKDNNS 372  
 QY 372 IITRKEFOELKTFPGVSGFEGESILFHYTDVDDORPENRYEALGDVVDGNFICPAL 431  
 DB 373 IITRKEFOELKTFPGVSGFEGESILFHYTDVDDORPENRYEALGDVVDGNFICPAL 432  
 QY 432 EPTKKPSEMNNAFFYFFFEHRSKSLPMPWGMVGHGEIEFVGLPLERDNTYKAEIL 491  
 DB 433 EPTKKPSEMNNAFFYFFFEHRSKSLPMPWGMVGHGEIEFVGLPLERDNTYKAEIL 492  
 QY 492 SRSIVKMANFAKYGNPNETONNSTMPVEFKSTEOKYTLTNTSESTRIMTKLRAQOQCRFWT 551  
 DB 493 SRSIVKMANFAKYGNPNETONNSTMPVEFKSTEOKYTLTNTSESTRIMTKLRAQOQCRFWT 552  
 QY 552 SFPKYLEMTGNTIDAEWEWKAGFHRNNYMMQNDWKQFNDYTSKESCVG 602  
 DB 553 SFPKYLEMTGNTIDAEWEWKAGFHRNNYMMQNDWKQFNDYTSKESCVG 603

RESULT 4

ACRYE  
 acetylcholinesterase (EC 3.1.1.7) precursor, 11S form [validated] - Pacific electric ray  
 N:Alternate names: acetylcholinesterase, asymmetric form  
 C:Species: Torpedo californica (Pacific electric ray)  
 C:Date: 17-Mar-1987 #sequence revision 08-Nov-1996 #text\_change 09-Jul-2004  
 A:Accession: A00773; A60820; A31962; B31962; B41117; S15677  
 R:Schunacher, M.; Camp, S.; Maule, Y.; Newton, M.; Macphree-Guigley, K.; Taylor, S.S.; Fr  
 Nature 319, 407-409, 1986  
 A:Title: Primary structure of Torpedo californica acetylcholinesterase deduced from its c  
 A:Reference number: A00773; MUID:86118676; PMID:3753747  
 A:Accession: A00773  
 A:Molecule type: mRNA  
 A:Residues: 'NS', 11-596 <SCH>  
 A:Cross-references: UNIPROT:P04058; GB:X03439; NID:964389  
 A:Experimental source: electric organ  
 A:Note: parts of this sequence, including the amino and carboxyl ends of the mature prote  
 R:Schunacher, M.; Camp, S.; Maule, Y.; Newton, M.; Macphree-Guigley, K.; Taylor, S.S.; Fr  
 Fed. Proc. 45, 2376-2381, 1986  
 A:Title: Primary structure of acetylcholinesterase: implications for regulation and functi

A:Reference number: A60820; MUID:87054662; PMID:3536598  
 A:Accession: A60820  
 A:Status: nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 22-596 <SC2>  
 R:Schumacher, M.; Maule, Y.; Camp, S.; Taylor, P.  
 J. Biol. Chem. 263, 18979-18987, 1988  
 A:Title: Multiple messenger RNA species give rise to the structural diversity in acetylcholinesterase  
 A:Reference number: A92701; MUID:89066695; PMID:3198606  
 A:Accession: A31962  
 A:Molecule type: mRNA  
 A:Residues: 1-23 <SC3>  
 A:Cross-references: EMBL:X03439; NID:964389  
 A:Experimental source: clones AChE-11 and AChE-18  
 A:Note: revision to sequence A00773  
 A:Accession: B31962  
 A:Molecule type: DNA, mRNA  
 A:Residues: 499-565 <SC4>  
 A:Cross-references: GB:X03439; NID:964389  
 A:Experimental source: Clone AChE-1  
 R:MacPhee-Quigley, K.; Taylor, P.; Taylor, S.  
 J. Biol. Chem. 260, 12185-12189, 1985  
 A:Title: Primary structures of the catalytic subunits from two molecular forms of acetylcholinesterase  
 A:Reference number: A23902; MUID:86008285; PMID:3900071  
 A:Accession: A23902  
 A:Molecule type: protein  
 A:Residues: 22, 'B', 24-45; 214-237 <MAC>  
 A:Note: active site Ser identification  
 R:Kreienkamp, H.U.; Weise, C.; Raba, R.; Aayksee, A.; Huch, F.  
 Proc. Natl. Acad. Sci. U.S.A. 88, 6117-6121, 1991  
 A:Title: Amino acid residues of the catalytic center of acetylcholinesterase from Torpedo  
 A:Reference number: A41117; MUID:91296772; PMID:2068091  
 A:Accession: B41117  
 A:Molecule type: protein  
 A:Residues: 100-108 <KRE>  
 A:Note: substrate binding site  
 R:Maule, Y.; Camp, S.; Gibney, G.; Rachinsky, T.L.; Ekstrom, T.J.; Taylor, P.  
 Neuron 4, 289-301, 1990  
 A:Title: Single gene encodes glycopospholipid-anchored and asymmetric acetylcholinesterase  
 A:Reference number: F50113; MUID:90166618; PMID:2306366  
 A:Accession: S15677  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 557-596 <MAU>  
 A:Cross-references: EMBL:X56516  
 R:MacPhee-Quigley, K.; Vedvick, T.S.; Taylor, P.; Taylor, S.S.  
 J. Biol. Chem. 261, 13565-13570, 1986  
 A:Title: Profile of the disulfide bonds in acetylcholinesterase.  
 A:Reference number: A43099; MUID:87008586; PMID:3759980  
 A:Contents: annotation; disulfide bonds  
 R:Susman, J.L.; Harel, M.; Silman, I.  
 submitted to the Brookhaven Protein Data Bank, October 1991  
 A:Reference number: A50061; PDB:1ACE  
 A:Contents: annotation; X-ray crystallography, 2.8 angstroms, residues 26-481, 511-555 of R:Susman, J.L.; Harel, M.; Frolow, F.; Oefner, C.; Goldman, A.; Tokar, L.; Silman, I.  
 Science 253, 872-879, 1991  
 A:Title: Atomic structure of acetylcholinesterase from Torpedo californica: a prototypic AChE  
 A:Contents: annotation; X-ray crystallography, 2.8 angstroms, residues 26-481, 511-555 of R:Susman, J.L.; Harel, M.; Frolow, F.; Oefner, C.; Goldman, A.; Tokar, L.; Silman, I.  
 C:Comment: Synapses usually contain this 11S (asymmetric) form of cholinesterase with a holoesterase occurs on the outer surfaces of cell membranes, including those of erythrocytes  
 C:Complex: 11S form is disulfide linked homodimer; 18S form is homotetramer, a dimer of C:Function:  
 A:Description: hydrolyzes acetylcholine to choline and acetate  
 A:Pathway: neurotransmitter degradation  
 C:Superfamily: cholinesterase; cholinesterase homology  
 C:Keywords: alternative splicing; carboxylic ester hydrolase; glycoprotein; membrane protein  
 F:1-21/DNA: signal sequence #status predicted <SIG>  
 F:22-596/Product: acetylcholinesterase, 11S form #status experimental <MAT>  
 F:51-551/DNA: cholinesterase homology <CHS>  
 F:80-478, 554/Binding site: carbohydrate (asn) (covalent) #status predicted  
 F:88-115, 275-286, 423-542/Disulfide bonds: #status experimental  
 F:105/Binding site: substrate (Trp) #status experimental

F:221/Active site: Ser #status experimental  
 F:348, 461/Active site: Glu, His #status predicted  
 F:437/Binding site: carbohydrate (asn) (covalent) #status experimental  
 F:593/Disulfide bonds: interchain #status experimental

Query Match 55.0%; Score 1791.5; DB 1; Length 596;  
 Best Local Similarity 53.2%; Pred. No. 5, 1e-129;  
 Matches 314; Conservative 111; Mismatches 160; Indels 5; Gaps 3;

13 LWFLLLCMLICKSHEDDIIATKNGKRGKGLVFGSTVAFPGIPAPQPLRLRPK 72  
 12 LHLVVLCO-ADDSSE-LIVNTSGKMGTRVPLSHISAFGLIPAEPPVGMKFR 67  
 73 KPSLTLMKMDINWATKYANCCONIDQSPGFHSGEMNPNITLSEDCILYINWIPAPK 132  
 68 REPPEKPKMGVWNAATYPPNCCQYDEQPGFSGSEMNPNNEMSEDCILYINWIPSPR 127  
 133 KNATVILWYGGGPGTGTSSLHYDQKFLARVERIVVSMYRVGALGLALPGNPEAPG 192  
 128 KSTYVWVWYGGGPGFYSSTLDVYNGKYLAYTEEVVLSYRVAGFGLALHSGQEAAG 187  
 193 NMGLFPQQLALWQVKNITAPGKPKSVTLPGESAGASVSLHLSPGSHLFTBALLOS 252  
 188 NVGLLDQRMALQVHDNIQFPGSDPKYVTFESAGASVGMHILSPGSRDLFRALLOS 247  
 253 GSFNAPWATSLYEARNFTLNLAKLTGCSRENETELIKLRNKDQELINAEFVVPYGT 312  
 248 GSNPCWASVSVAGEGRRAVELGRNLNGLNDELHCLREKKQDELIDVENVLPFDS 307  
 313 PLVNFPGTVDDELTDMDPILIEQLQFKKTOILGVNKGDEGTFLVYAGAPPSKDNNSI 372  
 308 IFRFSVFPVYIDGFEFFPSTLESMLNSGNFKKTOILGVNKGDEGTFLLYAGAPPSKDSK 367  
 373 ITRKEFGELKTFEPVSEFGKSLFHTYTDWDDPRFENYBEALGDVYGVNFIQPALE 432  
 368 ISKEDMSGKLSVPRANDGLDVTLYOTTDWDDNGIKRNGDLDIDVHVICPLMH 427  
 433 FTKKPEMGWNAFFYFHERSSKLPWPEWGVWGEYIEFVGLPLERDNTYKAEILS 492  
 428 FVAKYKFGNGVLYFPNFRASNLVPEWVGVIHGEIEFVGLPLVKELANTAESEALS 487  
 493 RSTVKMANFAKGNENETQNNSTSPVKSSTEQKTLTINTESTRTMTLRQOQCFWTS 552  
 488 RRIHMYWATFAKGNENEPHOSKWPFLTYEQKIDINTETKMHQSLRFQVCFWNO 547  
 553 FPFKVLMTGNIDIEAEWEMWAGFRNNWMMDKNOFNNTYSKESCVGL 602  
 548 FLKFLNATETTIDEARQMKTEPHRMSYTMHMKQNFQHY-SHESCAEL 596

RESULT 5  
 A38868  
 acetylcholinesterase (EC 3.1.1.7) precursor - marbled electric ray  
 C:Species: Torpedo marmorata (marbled electric ray)  
 C:Date: 23-Apr-1993 #sequence, revision 15-Nov-1996 #ext\_change 09-Jul-2004  
 C:Accession: A38868; A29682; S15696; A25650  
 R:Massoulié, J.; Bon, S.  
 submitted to the EMBL Data Library, June 1992  
 A:Reference number: A38868  
 A:Accession: A38868  
 A:Molecule type: mRNA  
 A:Residues: 1-599 <MS>  
 A:Cross-references: UNIPROT:P07692; EMBL:X05497; NID:964414; PIDN:CA29047.1; PID:964415  
 R:Sikorav, J.L.; Krejci, E.; Massoulié, J.  
 EMBO J. 6, 1865-1873, 1987  
 A:Title: cDNA sequences of Torpedo marmorata acetylcholinesterase: primary structure of  
 A:Reference number: A29682; MUID:88004392; PMID:2820709  
 A:Accession: A29682  
 A:Molecule type: mRNA  
 A:Residues: 1-40, 'G', 42-226, 'G', 228-272, 'G', 274-284, 'E', 286-420, 'N', 422-599 <SIK>  
 A:Cross-references: EMBL:X05497  
 R:Sikorav, J.L.; Duval, N.; Anselmet, A.; Bon, S.; Krejci, E.; Legay, C.; Osterlund, M.;  
 EMBO J. 7, 2983-2993, 1988



Db 500 EKIFPAQRLMRYMANFARTGDPNBERDKAPQMPYTAQOQYVSLDRPLEVRKGLAQA 559  
Qy 547 CRFWTSFPPKYLEMTGNIDAEWEMKAGFHRMNNYMMDMKQFNDYTSKESCGVL 602  
Db 560 CAFMNRFLPKLSATDTLDEARQWKAEPHRSYVHWKQFDPHY-SKQERCSDL 614

## RESULT 7

JH0811  
acetylcholinesterase (EC 3.1.1.7) catalytic chain precursor - rat  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 09-Jul-2004  
C/Accession: JH0811  
R/Legay, C.; Bon, S.; Vernier, P.; Coussen, F.; Massoulie, J.  
J. Neurochem. 60, 337-346, 1993  
A/Title: Cloning and expression of a rat acetylcholinesterase subunit: generation of mul  
A/Reference number: JH0811; MUID:93107932; PMID:8417155  
A/Molecule type: mRNA  
A/Residues: 1-614 <LEGS>  
A/Cross-references: UNIPROT:P37136; GB:S50879; NID:g262092; P1DN:AA624586.1; PID:g262093  
A/Experimental source: striatum  
C/Comment: This protein is responsible for hydrolysis of acetylcholine at cholinergic sy  
C/Superfamily: cholinesterase; cholinesterase homology  
C/Keywords: carboxylic ester hydrolase; glycoprotein; membrane protein; muscle; nerve; n  
F:1-31/Domain: signal sequence #status predicted <SIG>  
F:32-614/Product: acetylcholinesterase catalytic chain #status predicted <MAT>  
F:63-569/Domain: cholinesterase homology <CHS>  
F:100-127,288-303,440-560/Disulfide bonds: #status predicted  
F:234,365,478/Active site: Ser, Glu, His #status predicted  
F:296,381,495/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 51.9%; Score 1693.5; DB 2; Length 614;  
Best Local Similarity 52.8%; Pred. No. 1.7e-121;  
Matches 315; Conservative 103; Mismatches 168; Indels 11; Gaps 5;  
Qy 16 FLILCMILIGKSHTE---DDIIATKXGKRYGMNLTVFGGVTAFGLIPYAOPPLGRLRF 71  
Db 19 FLILSLGCGARAGREDPOLIVVRGQRLGRLKAPGPVSFLGIPRAEPVSGRRF 78  
Qy 72 KKPSQLTKMSDINATKYANSCCONIDQSPFGHSEMMNNTDLSBDCYLVNVPAPK 131  
Db 79 MPPEPKPWSGILDTATTFQNVCYQYVDLTVPGFEGTEMMNPNRELSEDCYLVNWTYPR 138  
Qy 132 PKNAT-VLIWYGGGFGTGTSSLHYVDGKFLARVERIVVSMNRYGALGFLALPGNPEA 190  
Db 139 PTSEPTPLIWIYGGGFYSGASLDVYDGRFLAQVEGTVLVSMNRYGTFGFLALPGSREA 198  
Qy 191 PGNMGLFDQOLALQWVOKNIAAFGNPKSVTLFGESAGAAVSJHLSPGSHSLFTRAIL 250  
Db 199 PGNGLDQRLALQWVQENIAAFGDDPMSTVTLFGESAGAAVSQGHILSLPERSLPHRAVL 258  
Qy 251 QSGSFNPMWATVSLYEARNRTLNIAKLTCG---SRENETEIIKCLRNKQPOEILLNEAF 306  
Db 259 QSGFPGNPMWAVSGBARRATLLARLVGCPGAGGNDTELISCLTRRAQDLVDHBMH 318  
Qy 307 VVYGTPLSVNFGTVDGFLITMPDILLELQFRKQIILVGNKDEGTWLVYGAQFS 366  
Db 319 VLPQESIFRFSEFVVDGFLSDPDPDALINTGDFODQLVGVVXKDSYFLVYGVGFS 378  
Qy 367 KDNNSITTRKEFOGLKIFPPGVSEFKESILPHYTMDVDDQRENTREALGDVGVYNF 426  
Db 379 KDNSSLRSRAQFLAGVRIGVQASDLAAEAVVLAHYTMDLHPEDPAHLRDAASAVGDHNV 438  
Qy 427 ICPALFETKFSSEWGNNAFFYFPEHRSKLPWPEMGMVMEGYEIEFVFGJLERRDVYK 486  
Db 439 VCPYLAQLAGRLAAGARVAYVIFPHRASTLWPLMGVPHGYEIEFIFGLPLDSLVNTV 498  
Qy 487 AEELISLSYKRWANFAKGNPNETQNN-STSWPFKSTQKYLTLNTESTRITWTKLRAQ 545  
Db 499 EERIFARLQWYNTNIFATGDPNDRDSKSPRPWPYTTAAQOQYVSLNKLPLEVARGLRAQ 558

Qy 546 QCRFWTSFPPKYLEMTGNIDAEWEMKAGFHRMNNYMMDMKQFNDYTSKESCGVL 602  
Db 559 TCAPMNRFLPKLSATDTLDEARQWKAEPHRSYVHWKQFDPHY-SKQERCSDL 614

## RESULT 8

JH0314  
acetylcholinesterase (EC 3.1.1.7) precursor - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 12-Feb-1993 #sequence\_revision 12-Feb-1993 #text\_change 09-Jul-2004  
C/Accession: JH0314  
R/Rechinsky, T.L.; Camp, S.; Li, Y.; Ekstroem, T.J.; Newton, M.; Taylor, P.  
Neuron 5, 317-327, 1990  
A/Title: Molecular cloning of mouse acetylcholinesterase: tissue distribution of alternat  
A/Reference number: JH0314; MUID:90380429; PMID:2400605  
A/Accession: JH0314  
A/Molecule type: mRNA  
A/Residues: 1-614 <RAC>  
A/Cross-references: UNIPROT:P21836; EMBL:X56518; NID:g49844; P1DN:CAA39867.1; PID:g49845  
A/Experimental source: brain  
C/Superfamily: cholinesterase; cholinesterase homology  
C/Keywords: carboxylic ester hydrolase; glycoprotein; membrane protein; muscle; nerve; n  
F:1-31/Domain: signal sequence #status predicted <SIG>  
F:32-614/Product: acetylcholinesterase #status predicted <MAT>  
F:63-569/Domain: cholinesterase homology <CHS>  
F:100-127,288-303,440-560/Disulfide bonds: #status predicted  
F:234/Active site: Ser #status predicted  
F:296,381,495/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 51.9%; Score 1692.5; DB 2; Length 614;  
Best Local Similarity 52.1%; Pred. No. 2e-121;  
Matches 314; Conservative 106; Mismatches 172; Indels 11; Gaps 5;  
Qy 10 IRELFMFLILCMILIGKSHTE---DDIIATKXGKRYGMNLTVFGGVTAFGLIPYAOP 65  
Db 13 IAPPLFLILSLGCGARAGREDPOLIVVRGQRLGRLKAPGPVSFLGIPRAEP 72  
Qy 66 IGLRFRKKPSQLTKMSDINATKYANSCCONIDQSPFGHSEMMNNTDLSBDCYLVN 125  
Db 73 VGSRRFPPEPKPWSGILDTATTFQNVCYQYVDLTVPGFEGTEMMNPNRELSEDCYLVN 132  
Qy 126 WIDAPKPKNAT-VLIWYGGGFGTGTSSLHYVDGKFLARVERIVVSMNRYGALGFLAL 184  
Db 133 WTPYPPASPTPLIWIYGGGFYSGASLDVYDGRFLAQVEGTVLVSMNRYGTFGFLAL 192  
Qy 185 PGNPEAPGNMGLFDQOLALQWVOKNIAAFGNPKSVTLFGESAGAAVSJHLSPGSHSL 244  
Db 193 PGRREAPGNGLDQRLALQWVQENIAAFGDDPMSTVTLFGESAGAAVSQGHILSLPERSL 252  
Qy 245 FTRAILQSGSFNPMWATVSLYEARNRTLNIAKLTCG---SRENETEIIKCLRNKQPOE 300  
Db 253 FHRVAVLOSFPNPKPMWATVSGEARRATLLARLVGCPGAGGNDTELISCLTRRAQDL 312  
Qy 301 LLINEAPVYGTPLSVNFGTVDGFLITMPDILLELQFRKQIILVGNKDEGTWLVY 360  
Db 313 VDHBMHVLTPQESIFRFSEFVVDGFLSDPDPDALINTGDFODQLVGVVXKDSYFLVY 372  
Qy 361 GARGFSKDNNSITTRKEFOGLKIFPPGVSEFKESILPHYTMDVDDQRENTREALGDV 420  
Db 373 GVGFGSKDNSSLRSRAQFLAGVRIGVQASDLAAEAVVLAHYTMDLHPEDPAHLRDA 432  
Qy 421 VGVYNFICPALFETKFSSEWGNNAFFYFPEHRSKLPWPEMGMVMEGYEIEFVFGJLER 480  
Db 433 VGDHNVVCPYLAQLAGRLAAGARVAYVIFPHRASTLWPLMGVPHGYEIEFIFGLPLDP 492  
Qy 481 RDNVTKAEELISLSYKRWANFAKGNPNETQNN-STSWPFKSTQKYLTLNTESTRITW 539  
Db 493 SLNVTTERIFARLQWYNTNIFATGDPNDRDSKSPRPWPYTTAAQOQYVSLNKLPLEV 552  
Qy 540 TKLRAQCRFWTSFPPKYLEMTGNIDAEWEMKAGFHRMNNYMMDMKQFNDYTSKES 599  
Db 553 RGLRAQTCAPMNRFLPKLSATDTLDEARQWKAEPHRSYVHWKQFDPHY-SKQER 611





Db 485 RTEDPNDPRAPKAPQMPPTAGAOVSLMRPLRGVQASRAQAACAFMRFLKLNATD 544  
 Qy 563 NIDAEWEMWAKGFHRNNNMMDKNOFNDYTSKESCVGL 602  
 Db 545 TLDEARQWKAEPFRMSYVHWKNOGPDHY-SKQDRCSDL 583

## RESULT 11

S47639  
 acetylcholinesterase (EC 3.1.1.7) - chicken  
 C/Species: Gallus gallus (chicken)  
 C/Date: 25-Dec-1994 #sequence\_revision 10-Nov-1995 #text\_change 09-Jul-2004  
 C/Accession: S47639  
 R/Kendall, W.R.; Rimer, M.; Gough, N.R.  
 Biochim. Biophys. Acta 1218, 453-456, 1994  
 A/Title: Cloning and analysis of chicken acetylcholinesterase transcripts from muscle and  
 A/Reference number: S47639; MUID:94325359; PMID:8049273  
 A/Accession: S47639  
 A/Molecule type: mRNA  
 A/Residues: 1-767 <RAN>  
 A/Cross-references: UNIPROT:P36196; EMBL:U03472; NID:9623031; PIDN:AAA60456.1; PID:94241  
 C/Superfamily: cholinesterase; cholinesterase homology  
 C/Keywords: carboxylic ester hydrolase

Query Match 45.0%; Score 1466; DB 2; Length 767;  
 Best Local Similarity 38.9%; Pred. No. 6e-104;  
 Matches 298; Conservative 89; Mismatches 197; Indels 182; Gaps 7;

Qy 16 FLILCMILIGKSHTEDDII-----IATNGKVRGNLTV--FGGTVTAFLGIPYAO 64  
 Db 5 FLILLLILSPSTAHNFAYASAPRPREVTTGSRGLLPAGSGSTAAAFGLIPYAVP 64  
 Qy 65 PLGLRFRKKPOSL-TKMSDIWNAKTYANSCCONIDQSPFGHSEMMNPNTDLSDELTYL 123  
 Db 65 PLGLRFRPPPIPTPTWTGIRDAOOPACQWDTTFPFQSGEMNPNKREMSDELTYL 124  
 Qy 124 NWMTAPKPKNAATLWIMYGGGFGQTGSLHYVYDGKFLARVERIYVSMYRVGALFLA 183  
 Db 125 NWMTQKQDPTPEPVLWVYGGGFGGSLVDYVGRYLAALAEVAVSMYRVGSLFLA 184  
 Qy 184 LFGNPEAPGNMGLFDQOLALQWQNTAFAFGNPKSVTLFEGSAGAAVSLSHLILSPSHS 243  
 Db 185 LAGHRDAPGNVGLMDQRLAQWDMNAFAGDDELTLTFESAGAAVSFGHLLSPSHS 244  
 Qy 244 LFTTALLILOSFPNAPMAYTSLEYARNRTLANAKLTGSRKRENETIICKLRKDKOELLIN 303  
 Db 245 LFRRAVLQSGSPNGMWATIGAABGRRAAALGRAVGCYGNETELGCLRKEADADVLGG 304  
 Qy 304 EAFVVPSTPLSVNPGFTVDDPLTMDPDLLELGOF----- 340  
 Db 305 EGVNVPQSVRRFAFVAVDDGFVDSFDVAL-MGDIYVKGEGEGHGVGGDGGYGVKGG 363  
 Qy 341 ----- 340  
 Db 364 DGVKGVGGYGANGVREGDGGYGVKEGLREGYGVKEGYGVGDGANAYGARVPRPH 423  
 Qy 341 ----- 340  
 Db 424 RDETPPDAYGAKGADAYGAKAAPRPHDETS PDAYGAKMPRPRHDEASPDYTGAKMP 483  
 Qy 341 ----- 340  
 Db 484 RPHRDETPDAYGAKMPRPRHDETS PDAYGAKMPRPRHDEASPDYTGAKMP 483  
 Qy 377 EFOEGIKLFFPGVSEFGKESILFHTYDWDDQRPENYREALGDVVDYNTFCPALFTFK 436  
 Db 544 EFLGVRGVGPATLAAEAVVLTHTDLDADNPYKNEALDDIYGDHNVVCPILMAAFQOR 603  
 Qy 437 FSEWNNANFFYYFEHRSKSLPPEPMGVMGYEIFVYGLPLERDNTTKAEILSRIV 496  
 Db 604 WAORGKAYAYLFDHRSSTLLMPMSWGVPHGEIEFVGLPLEPNNYTRBEVLSRRIM 663

Qy 497 KEMANFAKYNENETONNNTSWPVEKSTOEKYLINTESTRIMTLRAQOCRFWTSFPEK 556  
 Db 664 KYMGAPARFGDNGV-GSPRWPPTPSGQRAHNAAPLPSGHGLRQICAFWTRFLPK 722  
 Qy 557 VLEMTGNIDEAEWEMWAKGFHRNNNMMDKNOFNDYTSKESCVGL 602  
 Db 723 LTNATGPPEDAEREWRLFEFRMSYVHWKNOGPDHY-SKQDRCSDL 767

## RESULT 12

A54413  
 acetylcholinesterase (EC 3.1.1.7) A precursor - Caenorhabditis elegans  
 C/Species: Caenorhabditis elegans  
 C/Date: 09-Sep-1994 #sequence\_revision 09-Sep-1994 #text\_change 09-Jul-2004  
 C/Accession: A54413; T29824  
 R/Arpaug, M.; Pedon, Y.; Cousin, X.; Chateonnet, A.; Berge, J.B.; Fournier, D.; Toutant, J. Biol. Chem. 269, 9957-9965, 1994  
 A/Title: cDNA sequence, gene structure, and in vitro expression of ace-1, the gene encodi  
 A/Reference number: A54413; MUID:94193691; PMID:8144590  
 A/Accession: A54413  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-620 <ARP>  
 A/Cross-references: UNIPROT:P38433; GB:X75331; NID:9475060; PIDN:CAA53080.1; PID:9671831  
 R/Wu, X.; Le, T.T.  
 submitted to the EMBL Data Library, May 1996  
 A/Description: The sequence of C. elegans cosmid w09b12.  
 A/Reference number: Z20693  
 A/Accession: T29824  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 1-620 <WUX>  
 A/Cross-references: EMBL:U58731; PIDN:AA00593.1; GSPDB:GN00028  
 A/Experimental source: strain Bristol N2; clone w09b12  
 C/Genetic: A;Map position: X  
 A;Gene: CESP:ace-1  
 A;Intons: 13/3; 59/2; 154/2; 236/3; 296/2; 454/2; 509/2; 573/1; 606/2  
 A/Superfamily: cholinesterase; cholinesterase homology  
 C/Keywords: carboxylic ester hydrolase  
 F/45-567/Domain: cholinesterase homology <CHE>

Query Match 35.0%; Score 1142; DB 2; Length 620;  
 Best Local Similarity 41.0%; Pred. No. 2.8e-79;  
 Matches 243; Conservative 94; Mismatches 213; Indels 42; Gaps 14;

Qy 46 LITPGGTVAFLGIPYAPPLGRLRKKPOSLTKMSDINNAKTYANSCCONIDQSPFGH 105  
 Db 35 LSQTGRPLTRFGIIPAEPPVGNLRKPKPKQPMRIPLNATTPNSCTQSEDYTGDFY 94  
 Qy 106 GSEMMNPNTDLSDELTYLWVIPA--PKPKATVLIWYGGFGQTGSLHYVYDGKFLA 162  
 Db 95 GSTMKNANTLSDELTYLWVYVGVKXDPNKKLA-WWVYVGGFGSGTALDYDGRILL 153  
 Qy 163 RVERIVSNMYRVGALGFLALPNDPAPGNMGLFDQOLALQWQNTAFAFGNPKSVTL 222  
 Db 154 VRENVILVANNYRVSIFGFLYM-NRPEADPNMGMQOLAMKVVHNKIIDIFGDLIRTL 212  
 Qy 223 FGSAGAAVSLSHLILSPSHSFTTALLILOSFPNAPMAYTSLEYARNRTLANAKTGS- 281  
 Db 213 FGSAGAAVSLSHLILSPSHSPYFHRALIOSGSTSPALPRDVALARAVILYNMAKCN 272  
 Qy 282 -----RENETIICKLRKDKOELLINAE-AFVVPSTPLSVNPGFTVDDPLTMDPDLLE 336  
 Db 273 MSLLNPYDILDLCFGAADDALRENMKAPVREFG---DEPWVPYVDGDFLLENAQTSLK 329  
 Qy 337 LGQFKTKQILIVGNKDEGTWFLYVYGAFGSKNNNSITTRKEFOGLKIFPGVSEFGKES 336  
 Db 330 QGNFKTKQLAGSNRDESIYFLTYQLPDIFPVAD-FFTKDFDKDLQWTKGVYDILPRQ 388  
 Qy 397 IL-----FHTYDW-DQRPENYREALGDVVDYNTFCALFTFKFSEWNNANFF 446  
 Db 389 ILKQQLTLAAVLAHREPODLVPTPRDWINMDKQGDYHFTGCVNEALAHYHGGDYY 448

447 YYPEHSSKLLPWPBMGMVGHGIEIEFVGLPL-ERRDNYTKABELSRIVKRWANPAKY 505  
449 YYPFHRSQOTWPMWGMVGHGIEINFIPEGELNKRPNYTOBERELSRFRVYANPAKT 508  
506 GNPENONNSTS---WPFVSTBEOKYTLTNTST---RIMTKLRAOQCFWTSFPPKV 557  
509 GDPKNKNDGSEFTQVWPKYNSVSMWMMVSSPKMKRIGHGPRRKECAFWRKAYLPL 568  
558 LEMTGNIDAEWEMKAGFHRW-NNYMMDKMGQFNDY-----TSKESGCG 601  
569 MAADVADGDPYLVKQMDKQNEITDMQYHFOYKRYQTYRQSDSETCG 620

RESULT 13  
S66236  
acetylcholinesterase (EC 3.1.1.7) precursor - yellow fever mosquito  
C:Species: Aedes aegypti (yellow fever mosquito)  
C>Date: 14-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004  
C:Accession: S66236  
R:Anthony, N.; Rocheleau, T.; Moccilin, G.; Lee, H.J.; ffrench-Constant, R.  
FEBS Lett. 368, 461-465, 1995  
A:Title: Cloning, sequencing and functional expression of an acetylcholinesterase gene  
A:Reference number: S66236; MUID:95361924; PMID:763199  
A:Accession: S66236  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-637 <ANT>  
A:Cross-references: UNIPROT:Q9TX11  
C:Superfamily: cholinesterase homology  
C:Keywords: carboxylic ester hydrolase  
F:1-28/Domain: signal sequence #status predicted <SIG>  
F:29-637/Product: acetylcholinesterase #status predicted <MAT>  
F:57-594/Domain: cholinesterase homology <CHR>

Query Match 33.8%; Score 1075.5; DB 2; Length 637;  
Best Local Similarity 37.8%; Pred. No. 3.5e-74;  
Matches 227; Conservative 95; Mismatches 225; Indels 53; Gaps 8;

3 SKYITICIRFLFWLLCMLIGKSHTEDDIIATKNGKVMGLTVGCVTAFLGPIYA 62  
4 SAVVRLCCNMISLLCTIVISPVYGIPIRLVVOQSSGPIRGRSTMVIGREHVHNGVFA 63  
63 QPPLGRLPFKPKQSLTKWSDIWNATKYANSCCONIDSPFGHSEMMNPYTDSECLY 122  
64 KPPDGRFPKPKVPAEPMHGVLDATRLPSCIGERYEFPFAGEEMNPNTINSECLY 123  
123 LNWIPA-----PKRKATVLIWYGGGFQGTSSLH 154  
124 LNIWVPTKRLRHGRGLNFGNNDFYODDDDFQROHOSKGLAMLVWYGGGFMSGTSLD 183  
155 VYDGKFLARVRYIVVSMNRYVGLAFLAP---GNBPANMGLFPOQLALOWOKNIA 211  
184 VYNAMEMAAVGNVIVASMOQRVGSFGFFYLAPLYNDADAPNGVGLMDQALALRWLKENAK 243  
212 AFGGNPKSVTLFGESAGAASVSLHLSFGSHSLFTRAILQSGSFNAPAVTSLYEARNRT 271  
244 AFGDPLPILITFGESAGSSVSLHLSPTVGLSRGLGSGTINAAKSHMSAKALSYA 303  
272 LNTAKLTGCS---RENTEIILKLRNKDPOEILINAEFVVPYGTPLSVNFGPTVDGFL 327  
304 BALIDDCNCAVTLTKDNPVYVNMCMRVNDAKTISVQO--MNSYSGILGFPAPITIDGFM 361  
328 TDMEDILILEGQFKKTOILVGNKDEGTWPLVYG-AAGFSKDNNSIITRKFOGLKIF 386  
362 TADMTMLREANLEGVILVGSNDBEGYFLLYDFIDYFEDATATSLPRDKFLIMNTIF 421  
387 PGVSEFGKESILFHTYTDVDDQRENYREALGDVVDYNTFCPALFTFKKSEGNNAF 446  
422 SKASEPREALITFYOTGWSGNDGYQNOQYGRSVGDHFFICPTNERPALGLAEGASVY 481  
447 YYPEHSSKLLPWPBMGMVGHGIEIEFVGLPLERRDNYTKABELSRIVKRWANPAKY 506

482 YFTHRTSLIMGEWGMVGLHDEVEYIFGQPMNVSMQYRORERDLSRRMVLSEFARSG 541  
507 NPNETONNSTSWPVEFKSTBEOKYTLTNTSTRTIMTKLRAO-----GFWTSFPPKV 557  
542 NP---ALEGHWFPVYTKENITFYFNAGE---DDLKGEYKGRGPATACAFMNDPLPRL 595

RESULT 14  
JEO150  
acetylcholinesterase (EC 3.1.1.7) - house fly  
N:Alternate names: choline esterase I; cholinesterase; true cholinesterase  
C:Species: Musca domestica (house fly)  
C>Date: 02-Jun-1998 #sequence\_revision 10-Jul-1998 #text\_change 09-Jul-2004  
C:Accession: JEO150  
R:Huang, Y.; Qiao, C.L.; Williamson, M.S.; Devonshire, A.L.  
Chinese J. Biotechnol. 13, 258-263, 1997  
A:Title: Characterization of acetylcholinesterase gene from insecticide-resistant housefly  
A:Reference number: JEO150  
A:Accession: JEO150  
A:Molecule type: mRNA  
A:Residues: 1-691 <HUA>  
A:Cross-references: UNIPROT:O8MXC4; UNIPROT:O8MXC7; UNIPROT:O8MXC5; UNIPROT:O8MXC8; UNIPROT:O8MXC9  
C:Comment: This protein is the target site for the organophosphates and carbamates in insects  
C:Superfamily: cholinesterase; cholinesterase homology  
C:Keywords: carboxylic ester hydrolase  
F:81-691/Product: acetylcholinesterase #status predicted <MAT>  
F:108-645/Domain: cholinesterase homology <CHR>

Query Match 32.1%; Score 1045; DB 2; Length 691;  
Best Local Similarity 38.1%; Pred. No. 8.6e-72;  
Matches 230; Conservative 99; Mismatches 218; Indels 56; Gaps 13;

8 ICIRFLP--WFLLCMLIGKSHTEDDIIATKNGKVMGLTVGCVTAFLGPIYAOP 65  
59 IC-RGLPATTVILKRSALTSAMTDHLTVOITSGPVAGKSVYQGRVHVFTGIPAKP 117  
66 LGRLPFKPKQSLTKWSDIWNATKYANSCCONIDSPFGHSEMMNPYTDSECLYLVN 125  
118 VDDLRFPKPKVPAEPMHGVLDATRLPATCVGERVEYFPGSEEMNPNTINSECLYFMI 177  
126 WIPA-----PKRKATVLIWYGGGFQGTSSLH 154  
178 WAPAKARLRHGRGTNGEHSKTDODHLISATPQNTNGILPLIWIYGGGFMSGTSLD 237  
155 VYDGKFLARVRYIVVSMNRYVGLAFLP---ALPG-NPEAPNGMGLFPOQLALOWOKN 209  
238 IYNALMSAVGNVIVASFOYRLGAFGLHSPVMPGFEERAPGVNGLMDQALALRWLKEN 297  
210 IAAFGNPKSVTLFGESAGAASVSLHLSFGSHSLFTRAILQSGSFNAPAVTSLYEARN 269  
298 ARAFGNPKSVTLFGESAGSSVSLHLSPTVGLSRGLGSGTINAAKSHMSAKALSYA 357  
270 RLNLAKLTGCSR---ENETETIILKLRNKDPOEILINAEFVVPYGTPLSVNFGPTVDG 325  
358 IGRALVNDCAVTLFENPOAVACRQVDAKTISVQO--MNSYSGILSVPSAPITIDGA 415  
326 FLTMDPILILEGQFKKTOILVGNKDEGTWPLVYG-AAGFSKDNNSIITRKROGLKXI 384  
416 FLPADPMTLTKTADLSGYTLIGVNDGEGYFLLYDFIDYFDKDATSLPRDKLLEMAN 475  
385 FPGVSEFGKESILFHTYTDVDDQRENYREALGDVVDYNTFCPALFTFKKSEGNNA 444  
476 IFQASQAREALITFYOTGWSGNDGYQNOQYGRSVGDHFFICPTNERPALGLAEGASV 534  
445 FPFYFHHSSKLLPWPBMGMVGHGIEIEFVGLPLERRDNYTKABELSRIVKRWANPAK 504  
535 HYYFTHRTSLIMGEWGMVGLHDEVEYIFGQPLNNSIQRVPERELGKRLMSVLEFAK 594  
505 YGNPNETONNSTSWPVEFKSTBEOKYTLTNTSTRTIMTKLRAO-----AOCRFWTSFPPKVLEM 560  
595 SGNP---AVDGEEMPNKEDPVYVYFSTDEK--IEKIQGRPLAKRCSFNDYLPKRVSW 649  
561 TGN 563

Db 650 IGS 652

## RESULT 15

A25363 acetylcholinesterase (EC 3.1.1.7) precursor - fruit fly (*Drosophila melanogaster*)

C/Species: *Drosophila melanogaster*  
C/Date: 16-Aug-1988 #sequence\_revision 31-Dec-1988 #text\_change 09-Jul-2004

C/Accession: A25363; A33469  
R/Hall, L.M.C.; Splerer, P.

EMBO J. 5, 2949-2954, 1986

A/Title: The A locus of *Drosophila melanogaster*: structural gene for acetylcholinesterase  
A/Reference number: A25363; MUID:87080281; PMID:3024971

A/Accession: A25363

A/Molecule type: mRNA

A/Residues: 1-746 <HAL>

A/Cross-references: UNIPROT:P07140

A/Note: the authors translated the codon TGG for residue 18 as Cys and AGA for residue 2  
R/Fournier, D.; Karch, F.; Bride, J.M.; Hall, L.M.C.; Berge, J.B.; Splerer, P.

J. Mol. Biol. 210, 15-22, 1989

A/Title: *Drosophila melanogaster* acetylcholinesterase gene structure, evolution and muta  
C/Reference number: A33469; MUID:90064544; PMID:2511327

A/Accession: A33469

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 98-746 <FOU>

A/Cross-references: GB:X17572

C/Genetics:

A/Gene: FlyBase: Ace

A/Cross-references: FlyBase: FBgn0000024

A/Superfamily: cholinesterase; cholinesterase homology

C/Keywords: carboxylic ester hydrolase

F164-704/Domain: cholinesterase homology <CHB>

Query Match 32.0%; Score 1044; DB 2; Length 746;  
Best Local Similarity 37.9%; Pred. No. 1.1e-71;

Matches 222; Conservative 100; Mismatches 204; Indels 60; Gaps 12;

30 DDIITATNGKVRGMNLTVPFGCTYATPIGYPADPGLRPFKKPQSLTKWSDIMNATKY 89

138 DRLVAVTSSGPGVRSVTVQREYVHYTGIRYAPRVEDLRFKRPVPAEPHGVLDATGL 197

90 ANSCCONIDQSPFPGHSEMMNPNTDLSDDLTYLNVWIPAP----- 130

198 SATCQREYEFYFPGSSGEIMNPNTNSSEDCLYINWAPAKARLRHGGANGSGHPKQ 257

131 -----KPKQAT-----VLIMVGGGFQGTSSLHVYDGKFLARVERVIYVSNRYV 176

258 ADTDLHINGNPQNTTNGLPILIMVGGGFMTGSKTLDIYNADIMAAVGNIVASFOYRV 317

177 GALTGLAL-PGNP-----EARGNMGLEPOQALQWQVQKNAIFGSGNPSTVTLFGESAGA 230

318 GAFGLHLAPFEPSEFAEPAPGNVGLWDQALAIRLKNNAHFGGNPEMWTLLFGESAGSS 377

221 SVSLHLSPGSHSLFTRAILQGSFNAPWAVTSLEYARNRRLTNLAKLTGCS-----REN 284

378 SYNAQIMSPVTRGLVYKRGMSQGTNNAPMSHTSKAYE--IGKRLINDCNMNSMLKTN 435

285 ETEIKLRNKPQELILNEAFVYGTPLSVNPGTYDGDPLDMPIILLEGOFKKTQ 344

436 PAHVMSCKRSVDAKTISVQO--WNSYSGILSPSPAPITDGAFLPADPMTLMKTDLDKQYD 493

345 ILVGNKDEGTWFLVYG-AFGSKNNNSITTRKEQEGGLKIFFPVSVRFGKESILFHYTD 403

494 ILMGNVREGTYFLLYDFIDYDQDATALPRDKLTLEIMNNIFGATQAEERAILFYOTS 553

404 WYDDQRPENYREALGVVDYNIQPALEFTKKFSEMGNNAFYYFEHRSSTLPPWEMWG 463

554 WEGNGCYQN-QQOIGRAVDHFFTCPTTEYQAALERGSVHYFFTRHSTSLGEMWG 612

464 VMHGYIEFVFGLEPRRDNYTKAEILSRSTIVKMANFAKYNENETONNSTSPVRS 523

Db 613 VLMHGEIEYFGQPLNNLSQIRPVERELCKRMLSAVIFAKTGNPAQ--DGEEMPNFSK 669

QY 524 TEQKYLTLNTESTRTIMTKLR-----AQOCRFWTSFPFKYLEMTGNID 565

Db 670 EDPVYIYFSTDK--IEKLARGEPLARCSFMNDYLPKRSWAGTCD 713

## RESULT 16

UC7990 acetylcholinesterase (EC 3.1.1.7) 1 - green peach aphid

C/Species: *Myzus persicae* (green peach aphid)

C/Date: 10-Nov-2003 #sequence\_revision 10-Nov-2003 #text\_change 24-Nov-2003

C/Accession: UC7990

R/Nabeshima, T.; Kozaki, T.; Tomita, T.; Kono, Y.

Biochem. Biophys. Res. Commun. 307, 15-22, 2003

A/Title: An amino acid substitution on the second acetylcholinesterase in the pirimicarb-  
A/Reference number: UC7990; PMID:12849975

A/Accession: UC7990

A/Molecule type: mRNA

A/Residues: 1-664 <NAB>

A/Cross-references: GB:AF287291

A/Experimental source: Pirimicarb susceptible strain S14

C/Comment: This enzyme is a target for organophosphate and carbamate insecticides at the  
C/Keywords: AChE; acyl pocket; disulphide bond; insecticide resistance

A/Gene: MPAChEI

Query Match 31.9%; Score 1038.5; DB 2; Length 664;  
Best Local Similarity 37.9%; Pred. No. 2.6e-71;

Matches 214; Conservative 107; Mismatches 204; Indels 39; Gaps 12;

24 GKSHEDDIIATKNGKVRGMNLTVPFGCTYATPIGYPADPGLRPFKKPQSLTKWSDI 83

59 GVDPTDESPVAVTSSGMVQGYTKLIANREVRVYTGIRPAKRPVGPAPFRFRPAVADPWTGV 118

84 WNTTKYANGSCCONIDQSPFPGHSEMMNPNTDLSDDLTYLNVWIPAPK-----PKVA--- 135

119 LNAITRLPNTCYQRYRYFPGFVGEEMNPNTKLSSECLTYLNVIPKQKTRHSHNNAHNA 178

136 --TVLIMVGGGFQGTSSLHVYDGKFLARVERVIYVSNRYVAGALGLAL-PGNP--- 189

179 KIVLVWIIYGGGIMSGTSTLIDYDGLLATPDMVIMASQYRLGAGSLYLFELPEDSD 238

190 -AFGNGLFPOQALQWQVQKNAIFGSGNPSTVTLFGESAGASVSLHLSPGSHSLFTA 248

239 DARGNMGLEPOQALAIRLKNNAHFGGNPEMWTLLFGESAGSSVHLISPTRGVNRRG 298

249 ILOGGSFNAPWAVTSLEYARNRRLTNLAK--LTGCS-----RENTEIKLRNKPQEI 300

299 ILOGSVNAPWS---YMGGERAVDIAKGLLDCCNCNSTLDSNPATMSCKRAVDASTI 354

301 LNEAFVVPYGTPLSVNPGTYDGDPLDMPIILLEGOFKKTQIILVGNKDEGTWFLVY 360

355 --SKKQNNSSGILGFSAPATVDGVLPEHRPLMLAKANPSDIDILIGSLNAGTYFLLY 412

361 G-APGSKNNNSITTRKEQEGGLKIFFPVSVRFGKESILFHYDW-----VDDQRPENYRE 415

413 DFVDFPRTSATLPEKFEQIVNVIFKORTOLERAIIYQSGEMEKDDVDR--YSNKK 470

416 ALGDVVDYNIQPALEFTKKFSEMGNNAFYYFEHRSSTLPPWEMGVHMGYIEFVFG 475

471 QLSVVADVFPVCCNTLNFANIVSRGARVYIYFFTRHSDHLMGDMGVHLHGEMQYVFG 530

476 LPLERRDNYTKAEILSRSTIVKMANFAKYNENETONNSTSPVRSQKYLTLNTES 535

531 HPLMSPNPNARREDLSIRIMEAFTRSLGTGP---VSDDIDMPLVYESNPYIHHVMAAE 587

536 TRIMTKLPAQCCRFVTSFPFVZLE 559

588 LHVGYGPRAAECQFMNGFFPKIAQ 611

RESULT 17



A:Experimental source: clone Y4886A

C:Genetics:

A:Gene: CESP.Y4886A.8

A:Introns: 24/3; 58/2; 132/2; 241/2; 461/2; 514/2

C:Superfamily: cholinesterase; cholinesterase homology

Query Match 28.7%; Score 937; DB 2; Length 584;

Best Local Similarity 38.4%; Pred. No. 1.2e-63;

Matches 208; Conservative 93; Mismatches 205; Indels 36; Gaps 16;

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QY 34 IATKNGKVRGMNLTVFGGTVTAFLGIPYAOPPLGRLRFKKPQSLTKMSDIMNATKYANSC 93
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 34 VQKLGTVRGTESDHGKRVRSFLGVPFAPPPINEHRFKKPPARPMMNGTISANTLSPAC 93
QY 94 CQNIQSPFGFSGSEMMNPNTDLSDCLYLVNWIAPPRKNAATVLIWYGGGFGQTGSSL 153
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 94 FGGRSDYDPTFGSGSEMMNPNTDLSDCLYLVNWIAPPRKNAATVLIWYGGGFGGSPSL 152
QY 154 HYYDGKFLARVERIVYVSNRVGALGFLALPGNEAPRGMGLFDQOLALQVQKNIAPF 213
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 153 LLYDGKELATRGAVIVNINRVGPGYLF-L-DHEIDVPGMMGLDQOLALYIRDHIFSF 211
QY 214 GGNPKSVTLFGSAGASVSLHLSPGSHLFTRAIIQSGSFNAPMAVTSLYEARNETLN 273
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 212 GGNPARISLVGSAGASIVAHILAPASGLFQNGIIQSGSLDNKMSDSPRAKOKSTA 271
QY 274 LAKLTGSRNENETIICLNKPOEILNEAFVVPYG---TPLSV-----NGPVTVDG 325
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 272 LADLVGNCQTKITDQACLRN-TPAQLIDINWVGLNLEFPFAIVSKDNFFKHLDG- 329
QY 326 FLTMDPILLELGQFK-KTQIILVGNKDEGTWFLVYAGPFGSKDNNSI---ITRKEFOG 381
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 330 -----FIAREGYSTDVNLMEGINHDEGNFWNIYNAKFP-DKQSVRGLDRDEHFC 382
QY 382 LKIFPGVSEFGKESILFHYTD--WVDQRPEN-YREALGVGDYVNFICPALETFKFS 438
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 383 VDTAFVQPELVRAKYVSDPKCTDPKKTIDFTQVQNVQWGDYFFTCDSIFAHNYP 442
QY 439 EW-GN--NAFFYVEHRSKLPWEMGVMGHGEIEFVGLPLERRD-NYTKAEILSR 494
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 443 KMAQNSNVFVYFDQPSANPMPKWTGVHGEIEFVGLPLNTAGTYKEMDVSEK 502
QY 495 IYKRWANPAKYGNPNTQ-----NSTSWPVKSTEQ-KYLLNTESTRIMTKLRAQCR 548
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 503 VIDFWTTFANTGVSLKRAVGTQKIKWDRYDGTHTMMNITGSPFMQIBIKVBCD 562
QY 549 FW 550
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 563 LW 564

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RESULT 20

T42399 acetylcholinesterase (EC 3.1.1.7) - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004

C:Accession: T42399

R:Gausso, M.; Culetto, E.; Fedon, Y.; Combes, D.; Toutant, J.P.; Arpagaus, M.

submitted to the EMBL Data Library, June 1999

A:Accession number: Z22157

A:Accession: T42399

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-607 <GRA>

A:Cross-references: UNIPROT:O61459; EMBL:AF039650; PIDN:AAAC14022.2

C:Genetics:

A:Gene: ace-3

C:Superfamily: cholinesterase; cholinesterase homology

C:Keywords: carboxylic ester hydrolase

Query Match 28.5%; Score 930; DB 2; Length 607;

Best Local Similarity 38.2%; Pred. No. 4.5e-63;

Matches 207; Conservative 93; Mismatches 206; Indels 36; Gaps 16;

```

QY 34 IATKNGKVRGMNLTVFGGTVTAFLGIPYAOPPLGRLRFKKPQSLTKMSDIMNATKYANSC 93
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 34 VQKLGTVRGTESDHGKRVRSFLGVPFAPPPINEHRFKKPPARPMMNGTISANTLSPAC 93
QY 94 CQNIQSPFGFSGSEMMNPNTDLSDCLYLVNWIAPPRKNAATVLIWYGGGFGQTGSSL 153
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 94 FGGRSDYDPTFGSGSEMMNPNTDLSDCLYLVNWIAPPRKNAATVLIWYGGGFGGSPSL 152
QY 154 HYYDGKFLARVERIVYVSNRVGALGFLALPGNEAPRGMGLFDQOLALQVQKNIAPF 213
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 153 LLYDGKELATRGAVIVNINRVGPGYLF-L-DHEIDVPGMMGLDQOLALYIRDHIFSF 211
QY 214 GGNPKSVTLFGSAGASVSLHLSPGSHLFTRAIIQSGSFNAPMAVTSLYEARNETLN 273
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 212 GGNPARISLVGSAGASIVAHILAPASGLFQNGIIQSGSLDNKMSDSPRAKOKSTA 271
QY 274 LAKLTGSRNENETIICLNKPOEILNEAFVVPYG---TPLSV-----NGPVTVDG 325
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 272 LADLVGNCQTKITDQACLRN-TPAQLIDINWVGLNLEFPFAIVSKDNFFKHLDG- 329
QY 326 FLTMDPILLELGQFK-KTQIILVGNKDEGTWFLVYAGPFGSKDNNSI---ITRKEFOG 381
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 330 -----FIAREGYSTDVNLMEGINHDEGNFWNIYNAKFP-DKQSVRGLDRDEHFC 382
QY 382 LKIFPGVSEFGKESILFHYTD--WVDQRPEN-YREALGVGDYVNFICPALETFKFS 438
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 383 VDTAFVQPELVRAKYVSDPKCTDPKKTIDFTQVQNVQWGDYFFTCDSIFAHNYP 442
QY 439 EW-GN--NAFFYVEHRSKLPWEMGVMGHGEIEFVGLPLERRD-NYTKAEILSR 494
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 443 KMAQNSNVFVYFDQPSANPMPKWTGVHGEIEFVGLPLNTAGTYKEMDVSEK 502
QY 495 IYKRWANPAKYGNPNTQ-----NSTSWPVKSTEQ-KYLLNTESTRIMTKLRAQCR 548
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 503 VIDFWTTFANTGVSLKRAVGTQKIKWDRYDGTHTMMNITGSPFMQIBIKVBCD 562
QY 549 FW 550
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 563 LW 564

```

RESULT 21

T33842 hypothetical protein Y44E3A.2 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004

C:Accession: T33842

R:Moessner, J.; Graves, T.; Kepler, D.

submitted to the EMBL Data Library, November 1998

A:Description: The sequence of C. elegans cosmid Y44E3A.

A:Reference number: Z21422

A:Accession: T33842

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-532 <MOE>

A:Cross-references: UNIPROT:O61371; EMBL:AF106589; PIDN:AACT8228.1; GSPDB:GN00019; CESP:Y

A:Experimental source: strain Bristol N2; clone Y44E3A

C:Genetics:

A:Gene: CESP.Y44E3A.2

A:Map position: 1

A:Introns: 16/3; 84/3; 143/2; 219/3; 298/3; 440/2

C:Superfamily: cholinesterase; cholinesterase homology

Query Match 27.4%; Score 893; DB 2; Length 532;

Best Local Similarity 40.8%; Pred. No. 2.5e-60;

Matches 201; Conservative 79; Mismatches 169; Indels 44; Gaps 16;

```

QY 47 TVFGGTVTAFLGIPYAOPPLGRLRFKKPQSLTKMSDIMNATKYANSCQNIQSPFGFSG 106
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 17 TPDGAKVSAPLGVYAKFPFGSRFFKMAEMIDNMSGELAKTIKCYLTIDSAFPQFPG 76

```

```

Qy 107 SEMNPTDISEDCLTYNVWIPAKPKXATYIMVYGGGFOTGSSSLHVVDGKRAVER 166
Db 77 AEMNNPPGASBEDCLNNTWV--PEBDHGSVMWVIYGGGFSTPSLDLYSGSVFAAKHE 134
Qy 167 VIVVMNVYRGALGFALPGNPEARGNMGFLPDQDLAQWYQKNIAAGFNPKSVTLFGE 226
Db 135 TIVVNVNVRILGPFGLYFGDDSPIGANNGLMDQDLALRWHEINICAFGDRSRVTLFGE 194
Qy 227 AGAASVSLHLSPGSHSLFTRAILQSGSFNAPPAVTSLEYEARNTLAKLTGSSRENET 286
Db 195 AGSASTTAHLPAAPNSHKYFPNNIAKSGSINSMSAPPTPTMLDLSFRALKVNCSSPDM 254
Qy 287 EIIICLRNKDQOEILINAEFV--PYGTPLSVNGP--TVDGDFLTMDPDLILELG--QFK 341
Db 255 AIVGCLSV--PAHLYQAEADNISGDIGPMTFAVYPSDANF--QGDVQKLANQFK 311
Qy 342 K-TQILVGNKDEGTFLVY--GAP--GFS-----KDNNSITTRKEFOEGLKTFP 387
Db 312 KDVNIIFGSVDEGTMYMLPYTMSLPKYGFAPNHTISADPHNRALLTRDHYESRAEMP 371
Qy 388 GVSEFGKSLIFHY-----TVMVDQRENTREALGDVGVNFIPLALBETFKSE 439
Db 372 YFA--GSLVYNAFMSYEHVSTSNVPER--YRDGVARLGLDLPFLCSLIDPADLISD 426
Qy 440 --WGNNAEFFYFEHRSSKLPMPKMWGVNHGYIEFVGLPLERRDNTYKA---EELISR 493
Db 427 NIFG-NVYMYFFYRRSSANPMPKMGVNHGYIEVAFQPYWRPHLYDQTLHLEKRLSS 485
Qy 494 SIVKRWANFAKYG 506
Db 486 IIMQIMAFANTG 498

```

RESULT 22  
A34329  
60K esterase (EC 3.1.1.-) isoform 2 - rabbit  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C:Date: 22-Jun-1990 #sequence\_revision 22-Jun-1990 #text\_change 09-Jul-2004  
C:Accession: A34329  
R:Ozols, J.  
J. Biol. Chem. 264, 12533-12545, 1989  
A:Title: Isolation, properties, and the complete amino acid sequence of a second form of  
A:Reference number: A34329; MUID:89308686; PMID:2745458  
A:Accession: A34329  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-532 <OZO>  
A:Cross-references: UNIPROT:P14943  
C:Superfamily: cholinesterase; cholinesterase homology  
C:Keywords: carboxylic ester hydrolase  
F:32-517//Domain: cholinesterase homology <CHP>  
F:201,430//Active site: Ser, His #status predicted

Query Match	23.1%;	Score 754;	DB 2;	Length 532;
Best Local Similarity	36.1%;	Pred. No. 1.1e-49;		
Matches 199; Conservative	90;	Mismatches 202;	Indels 60;	Gaps 22

Qy	36	TNKRVRKRMNLTIVGG--GTVTAFLGIPYAPQPLRLKPKQKSLTUKSDINNAKRYANSC	93
Db	10	THIQGVRSLVHVSTGADGVAHTFLGIPPAKRPPLGLRPAPEPBAAMSGVADGSLPAMC	69
Qy	94	CONT---DQSPFGPHGSEMMNPNTLSDCLYLVNWT--APKRNATVLTIWYGGGRQT	148
Db	70	LQNLAIMDQVILLHFTF---PSIPMSDCLYLINITYSPAHRBESDLPVMWIRGGGLTM	126
Qy	149	GTSSLHTVDGKFLARVERVIYVSMYRYGALGFLALPBNPAPNGMGLFDQQLALQWYQ	208
Db	127	GMAST--YDGSALAAFEVDVVVITQYRLGVGLGFFS--TGDQKATNGHGLDQVALRWQK	183
Qy	209	NIAAFGCGPKSVTLTEGESAGAASVLIHLSPGSSILFTRALTGSGSFNAAPAVSLYEAR	268
Db	184	NIAHGNGKGVTLTFGSAGCTSVSSHVLSPMISQGLFPGALIMESLVALPOLITSSSEV	243

```

QY      NRTNLALATGCSRNETETIIICLRNKDPOEIL-LNEAFVVPRTPLSVNFGPVDGFL 327
Db      269 STV--VANLSRCGVQVDSLTIVRCLRAKSEEMELATIQVFMILIG-----VVDGYFL 292
QY      244 TDMPDILLETGQFKTKQILVGVNKGEGTW----FLVYGAAPGSKDNNSIITRKPEFQGLK 383
Db      223 PRHPELLALADFOVVPSTIIGINNDEYGMIIPTLLALIDPQESRDQAM--REIMHQATX 350
QY      384 --IFPGVSEFKESILFHYTWDVDDQRPENYREALGDVVGDNVFI CPALEFTKFSBWC 441
Db      351 QLMLEPALGDL---LMDEYMGSNED--PKHLMAGQEMMADAMFVPAIR-VANLORSH 403
QY      442 NNAFFYYIEHNS--KLPMPEMMGVNMGYEIEVF-----GLPLEKRDNYTAAEELLS 492
Db      404 APTVEYEFQHRPSFTKDLRPPHVRADHGDEWVFVFGSHLFGSKVPL-----TDEEBELLS 457
QY      493 RSVRYEMNAPKYGPNERTQNNSTSWPVFKSTEOKLLTLNTESTRIMTKLRAOOCRFPTS 552
Db      458 RRVMTYMANFAENRPN--GBGLAHMPLF-DLDQRYQLMLMOPR-VGOALAKRRLQEWTH 513
QY      553 FFP-KYLEWTG 562
Db      514 TLDPQVQELRG 524

```

RESULT 23  
G39768  
Cholinesterase (EC 3.1.1.8) - rhesus macaque (fragment)  
C.Species: Macaca mulatta (rhesus macaque)  
C.Date: 14-Feb-1992 #sequence\_revision 14-Feb-1992 #text\_change 09-Jul-2004  
C.Accession: G39768  
R.Airgagnus, M.; Chatonnet, A.; Masson, P.; Newton, M.; Vaughan, T.A.; Bartels, C.F.; Nogu  
J. Biol. Chem. 266, 6566-6974, 1991  
A.Title: Use of the polymerase chain reaction for homology probing of butyrylcholinesterase  
A.Reference number: A39768; PMID:2016308  
A.Accession: G39768  
A.Status: preliminary  
A.Molecule type: DNA  
A.Residues: 1-141 <ARP>  
A.Cross-references: UNIPROT:P32751; GB:W62777; NID:g342078; PIDN:AAA36836.1; PID:g342079  
C.Superfamily: cholinesterase; cholinesterase homology  
C.Keywords: carboxylic ester hydrolase; glycoprotein  
F.1-141/Domain: cholinesterase homology (fragment) <CHE>

Query Match	23.1%	Score	753	DB 2	Length	141	
Best Local Similarity	100.0%	Pred. NO.	1.9e-50				
Matches	141	Conservative	0	Indels	0	Gaps	0
		Mismatches	0				

QY	96	NIDSPGFGHSEMMNNNTDISECLNTNWIPAPKPKNATVLIWIYGGGFQGTSSLAHV	155
Db	1	NIDSPGFGHSEMMNNNTDISECLNTNWIPAPKPKNATVLIWIYGGGFQGTSSLAHV	60
QY	156	YDGEKELARVERVIVVSMNRYGALGFTALPGNPEAPGNMGLFDQOLALQWVQKIIAAFGG	215
Db	61	YDGEKELARVERVIVVSMNRYGALGFTALPGNPEAPGNMGLFDQOLALQWVQKIIAAFGG	120
QY	216	NPKSVTLLFGESAGAASVSLHH	236
Db	121	NPKSVTLLFGESAGAASVSLHH	141

RESULT 24  
JC5408  
carboxylesterase (RC 3.1.1.1) - human  
C/Species: Homo sapiens (man)  
C/Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C/Accession: JC5408  
R/Schwer, H.; Langmann, T.; Daig, R.; Becker, A.; Aslanidis, C.; Schmitz, G.  
Biochem. Biophys. Res. Commun. 253, 117-120, 1997  
A/Title: Molecular cloning and characterization of a novel putative carboxylesterase, pre  
A/Reference number: JC5408; MUID:97289502; PMID:9144407  
A/Accession: JC5408  
A/Molecule type: mRNA







Thu Jan 6 10:14:55 2005

us-09-748-739a-2.rpr

Page 15

Search completed: January 6, 2005, 09:41:42  
Job time : 47 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

## OM protein - protein search, using sw model

Run on: January 6, 2005, 09:21:17 ; Search time 161 Seconds  
(without alignments)  
1341.336 Million cell updates/sec

Title: US-09-748-739A-2

Perfect score: 3260  
Sequence: 1 MDSKVITICIRFLFWFLLC.....MDWKQFNFDYTSKESCVGL 602

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729239 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 100 summaries

Database : A\_Geneseq\_23Sep04.\*

1: geneseq1980s.\*  
2: geneseq1990s.\*  
3: geneseq2000s.\*  
4: geneseq2001s.\*  
5: geneseq2002s.\*  
6: geneseq2003as.\*  
7: geneseq2003bs.\*  
8: geneseq2004s.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3260	100.0	602	5	AAOI8897 Human but
2	3239	99.4	602	3	AAV59235 Human but
3	3239	99.4	602	3	AAV49471 Human but
4	3239	99.4	602	3	AAV44573 Human but
5	3239	99.4	602	6	ABR62392 Human but
6	3239	99.4	602	7	ADP90908 Human but
7	3235	99.2	602	3	AAV44574 Human but
8	3234	99.2	602	3	AAV49483 Human but
9	3233	99.2	602	2	AAV37442 Human but
10	3232	99.1	602	3	AAV49474 Human but
11	3232	99.1	602	3	AAV49473 Human but
12	3232	99.1	602	3	AAV49475 Human but
13	3231	99.1	602	3	AAV49472 Human but
14	3231	99.1	602	3	AAV49476 Human but
15	3230	99.1	602	3	AAV49477 Human but
16	3228	99.0	602	3	AAV49484 Human but
17	3228	99.0	602	3	AAV49478 Human but
18	3227	99.0	602	3	AAV49485 Human but
19	3227	99.0	602	3	AAV49486 Human but
20	3227	99.0	602	3	AAV49488 Human but
21	3226	99.0	602	3	AAV49487 Human but
22	3225	98.9	602	3	AAV49482 Human but
23	3224	98.9	602	3	AAV49481 Human but
24	3223	98.9	602	3	AAV49480 Human but
25	3223	98.9	602	3	AAV49479 Human but

26	3110	95.4	574	7	ABW00722 Human but
27	3107	95.3	574	8	ADP01039 Human but
28	3103	95.2	574	8	ADP01047 Human but
29	3102	95.2	574	8	ADP01051 Human but
30	3102	95.2	574	8	ADP01035 Human but
31	3101	95.1	574	8	ADP01041 Human but
32	3100	95.1	574	8	ADP01037 Human but
33	3099	95.1	574	5	AAOI8944 Human but
34	3098	95.0	574	8	ADP01049 Human but
35	3096	95.0	574	5	AAE25235 Human but
36	3096	95.0	574	5	AAOI8982 Human but
37	3096	95.0	574	5	AAOI8898 Human but
38	3096	95.0	574	6	ABR62391 Human but
39	3096	95.0	574	7	ABW00695 Human but
40	3096	95.0	574	8	ADP44639 Human but
41	3096	95.0	574	8	ADP01077 Human but
42	3095	94.9	574	8	ADP01045 Human but
43	3093	94.9	574	8	ADP01059 Human but
44	3093	94.9	574	8	ADP01075 Human but
45	3092	94.8	574	5	AAOI8977 Human but
46	3092	94.8	574	7	ABW00723 Human but
47	3092	94.8	574	8	ADP01080 Human but
48	3091	94.8	574	5	AAOI8979 Human but
49	3091	94.8	574	5	AAOI8960 Human but
50	3090	94.8	574	5	AAOI8983 Human but
51	3090	94.8	574	5	AAOI8945 Human but
52	3090	94.8	574	5	ADP44833 Human but
53	3090	94.8	574	8	ADP01073 Human but
54	3089	94.8	574	5	AAOI8981 Human but
55	3089	94.8	574	5	AAOI8940 Human but
56	3089	94.8	574	8	ADP01079 Human but
57	3089	94.8	574	8	ADP01078 Human but
58	3088	94.7	574	7	ABW00724 Human but
59	3088	94.7	574	8	ADP44738 Human but
60	3088	94.7	574	8	ADP01055 Human but
61	3088	94.7	574	8	ADP01061 Human but
62	3088	94.7	574	8	ADP01065 Human but
63	3088	94.7	574	8	ADP01071 Human but
64	3088	94.7	574	8	ADP01069 Human but
65	3088	94.7	574	5	AAOI8978 Human but
66	3087	94.7	574	5	AAOI8978 Human but
67	3087	94.7	574	8	ADP01063 Human but
68	3087	94.7	574	8	ADP01043 Human but
69	3086	94.7	574	5	AAOI8942 Human but
70	3086	94.7	574	5	AAOI8941 Human but
71	3086	94.7	574	8	ADP44765 Human but
72	3086	94.7	574	8	ADP44821 Human but
73	3086	94.7	574	8	ADP01057 Human but
74	3086	94.7	574	5	AAOI8899 Human but
75	3085	94.6	574	5	AAOI8943 Human but
76	3085	94.6	574	5	AAOI8901 Human but
77	3085	94.6	574	5	AAOI8902 Human but
78	3085	94.6	574	8	ADP44800 Human but
79	3085	94.6	574	8	ADP44771 Human but
80	3085	94.6	574	5	AAOI8976 Human but
81	3084	94.6	574	5	ADP44776 Human but
82	3084	94.6	574	8	ADP44810 Human but
83	3084	94.6	574	8	ADP44758 Human but
84	3084	94.6	574	8	ADP44780 Human but
85	3084	94.6	574	8	ADP44806 Human but
86	3084	94.6	574	8	ADP01053 Human but
87	3084	94.6	574	8	ADP44762 Human but
88	3083	94.6	574	8	ADP44769 Human but
89	3083	94.6	574	8	ADP44812 Human but
90	3083	94.6	574	8	ADP44770 Human but
91	3083	94.6	574	8	ADP44755 Human but
92	3083	94.6	574	8	ADP44772 Human but
93	3083	94.6	574	8	ADP44739 Human but
94	3083	94.6	574	8	ADP44744 Human but
95	3083	94.6	574	8	ADP44785 Human but
96	3083	94.6	574	8	ADP44785 Human but
97	3083	94.6	574	8	ADP44785 Human but
98	3082	94.5	574	5	AAOI8960 Human but

99 3082 94.5 574 5 AAO18971  
100 3082 94.5 574 5 AAO18933

## ALIGNMENTS

## RESULT 1

AAO18897 standard; protein; 602 AA.

XX AAO18897;  
XX  
XX 02-DEC-2002 (first entry)  
XX  
XX Human butyrylcholinesterase variant #1.  
XX  
XX Human; butyrylcholinesterase; enzyme; mutant; cocaine hydrolysis;  
XX cocaine addiction; antiaddictive; antidote.  
XX  
XX Homo sapiens.  
XX  
XX MO200264796-A2.  
XX  
XX 22-AUG-2002.  
XX  
XX 21-DEC-2001; 2001WO-US050450.  
XX  
XX 26-DEC-2000; 2000US-00748739.  
XX 20-DEC-2000; 2001US-00032233.  
XX  
XX (MOLE-) APPLIED MOLECULAR EVOLUTION INC.  
XX PA (UTNE-) UNIT NERBASKA MEDICAL CENT.  
XX  
XX Lockridge O, Watkins JD, Hancock JD;  
XX  
XX WPI: 2002-636633/68.  
XX  
XX N-PSDB; AAL49276.  
XX  
XX New human butyrylcholinesterase variant polypeptides, useful for treating  
XX cocaine-induced conditions.  
XX  
XX PS Claim 1; Fig 1; 150pp; English.  
XX  
XX The present invention relates to mutants of human butyrylcholinesterase.  
XX The enzymes have an increased cocaine hydrolysis activity and can be used  
XX for treating a cocaine-induced condition. The present sequence is a  
XX protein shown in the exemplification of the invention  
XX  
XX SQ Sequence 602 AA;

Query Match 100.0%; Score 3260; DB 5; Length 602;  
Best Local Similarity 100.0%; Pred. No. 5.1e-289;  
Matches 602; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSKVTITICIRFLFWFLICMLIGKSHTEDDIIATKNGKVGQMLTVFGGTVAFLGIP 60  
DB 1 MSKVTITICIRFLFWFLICMLIGKSHTEDDIIATKNGKVGQMLTVFGGTVAFLGIP 60  
QY 61 YAAPPIGRIRLFFKPKQSLTKMSDIWNAITKANSCCQNIIDSPFGFGSEMMNNTDLSBDC 120  
DB 61 YAAPPIGRIRLFFKPKQSLTKMSDIWNAITKANSCCQNIIDSPFGFGSEMMNNTDLSBDC 120  
QY 121 LYINWVTPAPKPKNAITVLMVGGSGPOTGSSLAHYDGEFLARVERVIYVSMNRYGALG 180  
DB 121 LYINWVTPAPKPKNAITVLMVGGSGPOTGSSLAHYDGEFLARVERVIYVSMNRYGALG 180  
QY 181 FLALPGNPEAPGNMGLFDQOLALQWYQKNTAFGAPKSVTLFGESAGAASVSLHLISFG 240  
DB 181 FLALPGNPEAPGNMGLFDQOLALQWYQKNTAFGAPKSVTLFGESAGAASVSLHLISFG 240  
QY 241 SHSLFTRAILIQSGSFNAPMAVTSLYEARNTLMLATLQSGRNEHEIICKLRNKPQEI 300  
DB 241 SHSLFTRAILIQSGSFNAPMAVTSLYEARNTLMLATLQSGRNEHEIICKLRNKPQEI 300

DB 241 SHSLFTRAILIQSGSFNAPMAVTSLYEARNTLMLATLQSGRNEHEIICKLRNKPQEI 300  
QY 301 LLINEAFVVPYGTPLSVNPGFTVDGDFLTDMPDILLEIGQFKTOILVGNKDEGTWFLVY 360  
DB 301 LLINEAFVVPYGTPLSVNPGFTVDGDFLTDMPDILLEIGQFKTOILVGNKDEGTWFLVY 360  
QY 361 GAPGFSKDNNSIITRKEFOEGKIFPPGVSEFGKESILFHYTWDVQDQRENNREALGDV 420  
DB 361 GAPGFSKDNNSIITRKEFOEGKIFPPGVSEFGKESILFHYTWDVQDQRENNREALGDV 420  
QY 421 VGDVNFICPALFETKSEEMGNNAFFYYFEHRSKLLPMEPMGMVHGIEFVGLPLER 480  
DB 421 VGDVNFICPALFETKSEEMGNNAFFYYFEHRSKLLPMEPMGMVHGIEFVGLPLER 480  
QY 481 RDNVTKAEIILSRGIVKMANFAKYGMPNETQNNSTSNPVRKSTQKYLTLNTESTRIMT 540  
DB 481 RDNVTKAEIILSRGIVKMANFAKYGMPNETQNNSTSNPVRKSTQKYLTLNTESTRIMT 540  
QY 541 KLRAGQCRFTWTSFFPKVLEMTGNIDEAEWEMKAGFHRNNYMMQKQFNDYTSKESCV 600  
DB 541 KLRAGQCRFTWTSFFPKVLEMTGNIDEAEWEMKAGFHRNNYMMQKQFNDYTSKESCV 600  
QY 601 GL 602  
DB 601 GL 602

## RESULT 2

AAV59235 standard; protein; 602 AA.

AAV59235;

27-MAR-2000 (first entry)

Human butyryl cholinesterase (BuChE) mutant.

XX Organophosphate; detoxification; esterase; acetylcholinesterase; AChE;  
XX butyrylcholinesterase; BuChE; carboxylesterase; CaE; sheep dip; human;  
XX nerve agent; organophosphorus acid anhydride; OPAA; mutant.  
XX

XX Homo sapiens.  
XX Synthetic.  
XX

XX US6001625-A.  
XX

XX 14-DEC-1999.  
XX

XX 19-MAY-1995; 95US-00446100.  
XX

XX 19-MAY-1995; 95US-00446100.  
XX

XX (USSA ) US SEC OF ARMY.  
XX

XX Broomfield CA, Lockridge O, Millard CB;  
XX

XX WPI: 2000-096137/08.  
XX

XX Enhancing the organophosphate detoxifying capabilities of esterases for  
XX the treatment of organophosphate poisoning.  
XX

XX Disclosure; Col 99-102; 64pp; English.  
XX

XX The invention provides a method of enhancing organophosphate detoxifying  
XX capabilities of esterases (either human acetylcholinesterases (AChE), that  
XX human butyrylcholinesterases (BuChE) and/or carboxylesterases (CaE)), that  
XX comprises substituting a histidine residue for 1 or more amino acid(s)  
XX within 6 Angstrom of an active site serine. The method may be used for  
XX enhancing organophosphate detoxifying capabilities of esterases (either  
XX human AChE, human BuChE and/or human CaE). The modified esterases may  
XX then be used to treat agricultural workers poisoned with organophosphates  
XX through contact with chemical such as sheep dips. They may also be used  
XX to treat military personnel contaminated by chemical weaponry such as

CC nerve agents. Additionally, the esterases may also be used to  
 CC decontaminate ground and buildings and equipment used to store, or  
 CC contaminated by organophosphates. The method produces esterases with  
 CC improved detoxification properties over naturally occurring  
 CC organophosphorus acid anhydride (OPAA) hydrolyzing enzymes. They are also  
 CC less likely to be inactivated by the OPAA

XX Sequence 602 AA;

Query Match 99.4%; Score 3239; DB 3; Length 602;  
 Best Local Similarity 99.7%; Pred. No. 4.3e-287;  
 Matches 600; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDSKVTIIICIRFLFWFLMLCMIGKSHTEDDIIATKNGKVRGNLTVFGSTVTAFLGIP 60  
 DB 1 MHSKVTIIICIRFLFWFLMLCMIGKSHTEDDIIATKNGKVRGNLTVFGSTVTAFLGIP 60  
 QY 61 YAOPLGLRFRKKQSLTKMSDIWNAATKYANSCCONIDQSPFGHSGEMNPNPTDLSDC 120  
 DB 61 YAOPLGLRFRKKQSLTKMSDIWNAATKYANSCCONIDQSPFGHSGEMNPNPTDLSDC 120  
 QY 121 LYLNWVLPAPKPKNAATLWIYGGGFOTGSSLAHYDQKFLARVERIVVSMYRVGALG 180  
 DB 121 LYLNWVLPAPKPKNAATLWIYGGGFOTGSSLAHYDQKFLARVERIVVSMYRVGALG 180  
 QY 181 FLALPGNPEAPGNMGLFDQOLALQWQKNIAPGPNPKSVTLFGESAGAASVSLHLSPG 240  
 DB 181 FLALPGNPEAPGNMGLFDQOLALQWQKNIAPGPNPKSVTLFGESAGAASVSLHLSPG 240  
 QY 241 SHSLFTRAIIQSGSFNAPMAVTSIYEARNRTLNLAKTGCSRENETEIIKCLRKNDPOEI 300  
 DB 241 SHSLFTRAIIQSGSFNAPMAVTSIYEARNRTLNLAKTGCSRENETEIIKCLRKNDPOEI 300  
 QY 301 LLINEAFVVPYGTPLSVNFGPTVDGDFLTMDPDLLELGQFKKQIQLVGANKDGTAFLLV 360  
 DB 301 LLINEAFVVPYGTPLSVNFGPTVDGDFLTMDPDLLELGQFKKQIQLVGANKDGTAFLLV 360  
 QY 361 GAGPFSKDNNSIITRKEFOGLKIFPGVSEFGKESILFHTDWVDDQRPENYREALGDV 420  
 DB 361 GAGPFSKDNNSIITRKEFOGLKIFPGVSEFGKESILFHTDWVDDQRPENYREALGDV 420  
 QY 421 VGDYNTICPALLETFKKSEWGNNAFFYYFEHRSSKLPWPMWGMGGEIEFVGLPLER 480  
 DB 421 VGDYNTICPALLETFKKSEWGNNAFFYYFEHRSSKLPWPMWGMGGEIEFVGLPLER 480  
 QY 481 RDNTYKBEILSRISIVKMANPARYGNPNETONNSTSPVKESTEOKYLTLNTESTRLMT 540  
 DB 481 RDNTYKBEILSRISIVKMANPARYGNPNETONNSTSPVKESTEOKYLTLNTESTRLMT 540  
 QY 541 KLRAGQCRFWTSFPKYLEMTGNIDEAEWEKAGFHRNNYMMDMKQFNQDYSKESCV 600  
 DB 541 KLRAGQCRFWTSFPKYLEMTGNIDEAEWEKAGFHRNNYMMDMKQFNQDYSKESCV 600  
 QY 601 GL 602  
 DB 601 GL 602  
 DB 601 GL 602

RESULT 3

AA49471  
 ID AA49471 standard; protein; 602 AA.

XX AA49471;

XX 27-MAR-2000 (first entry)

XX Human wild-type butyryl cholinesterase (BuChE).

XX Organophosphate; detoxification; esterase; acetylcholinesterase; AChE;

KM butyrylcholinesterase; BuChE; carboxylesterase; Cae; sheep dip; human;

XX nerve agent; organophosphorus acid anhydride; OPAA.

OS Homo sapiens.

XX US6001625-A.  
 XX 14-DEC-1999.  
 PD 19-MAY-1995; 95US-00446100.  
 XX 19-MAY-1995; 95US-00446100.  
 PR 19-MAY-1995; 95US-00446100.  
 XX (USSA ) US SEC OF ARMY.  
 PA Broomfield CA, Lockridge O, Millard CB;  
 PI WPI; 2000-096137/08.  
 DR Enhancing the organophosphate detoxifying capabilities of esterases for  
 XX the treatment of organophosphate poisoning.  
 PT Disclosure; Col 3-4; 64pp; English.

CC The invention provides a method of enhancing organophosphate detoxifying  
 CC capabilities of esterases (either human acetylcholinesterases (AChE), that  
 CC human butyrylcholinesterases (BuChE) and/or carboxylesterases (Cae)), that  
 CC comprises substituting a histidine residue for 1 or more amino acid(s)  
 CC within 6 Angstrom of an active site serine. The method may be used for  
 CC enhancing organophosphate detoxifying capabilities of esterases (either  
 CC human AChE, human BuChE and/or human Cae). The modified esterases may  
 CC then be used to treat agricultural workers poisoned with organophosphates  
 CC through contact with chemical such as sheep dips. They may also be used  
 CC to treat military personnel contaminated by chemical weaponry such as  
 CC nerve agents. Additionally, the esterases may also be used to  
 CC decontaminate ground and buildings and equipment used to store, or  
 CC contaminated by organophosphates. The method produces esterases with  
 CC improved detoxification properties over naturally occurring  
 CC organophosphorus acid anhydride (OPAA) hydrolyzing enzymes. They are also  
 CC less likely to be inactivated by the OPAA

XX Sequence 602 AA;

Query Match 99.4%; Score 3239; DB 3; Length 602;  
 Best Local Similarity 99.7%; Pred. No. 4.3e-287;  
 Matches 600; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDSKVTIIICIRFLFWFLMLCMIGKSHTEDDIIATKNGKVRGNLTVFGSTVTAFLGIP 60  
 DB 1 MHSKVTIIICIRFLFWFLMLCMIGKSHTEDDIIATKNGKVRGNLTVFGSTVTAFLGIP 60  
 QY 61 YAOPLGLRFRKKQSLTKMSDIWNAATKYANSCCONIDQSPFGHSGEMNPNPTDLSDC 120  
 DB 61 YAOPLGLRFRKKQSLTKMSDIWNAATKYANSCCONIDQSPFGHSGEMNPNPTDLSDC 120  
 QY 121 LYLNWVLPAPKPKNAATLWIYGGGFOTGSSLAHYDQKFLARVERIVVSMYRVGALG 180  
 DB 121 LYLNWVLPAPKPKNAATLWIYGGGFOTGSSLAHYDQKFLARVERIVVSMYRVGALG 180  
 QY 181 FLALPGNPEAPGNMGLFDQOLALQWQKNIAPGPNPKSVTLFGESAGAASVSLHLSPG 240  
 DB 181 FLALPGNPEAPGNMGLFDQOLALQWQKNIAPGPNPKSVTLFGESAGAASVSLHLSPG 240  
 QY 241 SHSLFTRAIIQSGSFNAPMAVTSIYEARNRTLNLAKTGCSRENETEIIKCLRKNDPOEI 300  
 DB 241 SHSLFTRAIIQSGSFNAPMAVTSIYEARNRTLNLAKTGCSRENETEIIKCLRKNDPOEI 300  
 QY 301 LLINEAFVVPYGTPLSVNFGPTVDGDFLTMDPDLLELGQFKKQIQLVGANKDGTAFLLV 360  
 DB 301 LLINEAFVVPYGTPLSVNFGPTVDGDFLTMDPDLLELGQFKKQIQLVGANKDGTAFLLV 360  
 QY 361 GAGPFSKDNNSIITRKEFOGLKIFPGVSEFGKESILFHTDWVDDQRPENYREALGDV 420  
 DB 361 GAGPFSKDNNSIITRKEFOGLKIFPGVSEFGKESILFHTDWVDDQRPENYREALGDV 420  
 QY 421 VGDYNTICPALLETFKKSEWGNNAFFYYFEHRSSKLPWPMWGMGGEIEFVGLPLER 480  
 DB 421 VGDYNTICPALLETFKKSEWGNNAFFYYFEHRSSKLPWPMWGMGGEIEFVGLPLER 480

Db 421 VGDYNICPALLEFTKFSWGNNAFFYYFEHRSSKLPMPBMGVHGEIIEFVGLPLER 480  
 QY 481 RDNYTKAEELLSIVKRWANPAKYGNPNTONNSTNPFVKSTEQKYLTLNTESTRIMT 540  
 Db 481 RDNYTKAEELLSIVKRWANPAKYGNPNTONNSTNPFVKSTEQKYLTLNTESTRIMT 540  
 QY 541 KLRAGQCRFTWTSFPFKYLEMTGNIDEAEWEMKAGFHRMNNYMMDMKQFNDYTSKESCV 600  
 Db 541 KLRAGQCRFTWTSFPFKYLEMTGNIDEAEWEMKAGFHRMNNYMMDMKQFNDYTSKESCV 600  
 QY 601 GL 602  
 Db 601 GL 602

RESULT 4  
 AAY44573  
 ID AAY44573 standard; protein; 602 AA.

AC AAY44573;

DT 04-APR-2000 (first entry)

DE Human wild type Butyrylcholinesterase (BChE) protein.

XX Butyrylcholinesterase; BChE allele; neurological disease; treatment;  
 KM therapy; allelic variant; BChE-K; APOE4 allele; neurofibromatosis;  
 KM non-AD neurological disease; Alzheimer's disease; Huntington's disease;  
 KM depression; amyotrophic lateral sclerosis; multiple sclerosis; stroke;  
 KM Parkinson's disease; multi-infarct dementia; human.

OS Homo sapiens.

PN W09966072-A2.

PD 23-DEC-1999.

PE 16-JUN-1999; 99WO-IB001298.

PR 16-JUN-1998; 98US-0089406P.

PA (NOVA-) NOVA MOLECULAR INC.

PI Sevigny P, Wiebusch H, Schappert K;

DR WPI; 2000-126550/11.

DR N-PSDB; AAZ49470.

PT Prediction of drug efficacy for treating neurological diseases like

PT Alzheimer's disease, neurofibromatosis, Huntington's disease.

PS Example 1; Fig 3; 37pp; English.

XX The present sequence is the wild type human butyrylcholinesterase (BChE)  
 CC protein. Determining BChE allele status of a patient helps predicting  
 CC risk for neurological diseases, efficacy of therapy and determining  
 CC treatment protocol. Presence of BChE allelic variant, BChE-K and APOE4  
 CC allele indicate patient's risk for having a neurological disease. This  
 CC method enables treating Alzheimer's disease, depression,  
 CC neurofibromatosis, Huntington's disease, amyotrophic lateral sclerosis,  
 CC multiple sclerosis, stroke, Parkinson's disease, multi-infarct dementia  
 CC and other non-AD neurological diseases

XX Sequence 602 AA;

Query Match 99.4%; Score 3239; DB 3; Length 602;

Best Local Similarity 99.7%; Pred. No. 4.3e-287;

Matches 600; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDSKTTTICIRPLFWFLMLIGKSHEDDIIATKNGKVGKMLTVFGGTVTAFLGIP 60  
 Db 1 MDSKTTTICIRPLFWFLMLIGKSHEDDIIATKNGKVGKMLTVFGGTVTAFLGIP 60

QY 61 YAOPLGLRLFKKPSOLTKMSDINWATKYANSCCNIDQSFEGHSGEMNPNLSEDC 120  
 Db 61 YAOPLGLRLFKKPSOLTKMSDINWATKYANSCCNIDQSFEGHSGEMNPNLSEDC 120  
 QY 121 LYINWITPAPKRNATVLWIIYGGGQRTSSLAHYDGFLLARVRVIVSNMYVGAIG 180  
 Db 121 LYINWITPAPKRNATVLWIIYGGGQRTSSLAHYDGFLLARVRVIVSNMYVGAIG 180  
 QY 181 FLALPGENPAPGNMGLFDQQLALQWQKNIAPFGNPKSVTLFGESAGAASVSLHLSBG 240  
 Db 181 FLALPGENPAPGNMGLFDQQLALQWQKNIAPFGNPKSVTLFGESAGAASVSLHLSBG 240  
 QY 241 SHSLFTRAILQSGSFNAPMAVTSIYEARNRTINLAKITGCSRENETEIIKCLRNDPOEI 300  
 Db 241 SHSLFTRAILQSGSFNAPMAVTSIYEARNRTINLAKITGCSRENETEIIKCLRNDPOEI 300  
 QY 301 LLINEAFVVEYGTPLSVNPGPTVDGDELTMDDILLEIQGFKTQIILVGNKDEGTMLVY 360  
 Db 301 LLINEAFVVEYGTPLSVNPGPTVDGDELTMDDILLEIQGFKTQIILVGNKDEGTMLVY 360  
 QY 361 GAPGFSKDNNSIITRKEFOEGLKIFPPGVSEFGKESILFHYTDWDDQRPENYREALGDV 420  
 Db 361 GAPGFSKDNNSIITRKEFOEGLKIFPPGVSEFGKESILFHYTDWDDQRPENYREALGDV 420  
 QY 421 VGDYNICPALLEFTKFSWGNNAFFYYFEHRSSKLPMPBMGVHGEIIEFVGLPLER 480  
 Db 421 VGDYNICPALLEFTKFSWGNNAFFYYFEHRSSKLPMPBMGVHGEIIEFVGLPLER 480  
 QY 481 RDNYTKAEELLSIVKRWANPAKYGNPNTONNSTNPFVKSTEQKYLTLNTESTRIMT 540  
 Db 481 RDNYTKAEELLSIVKRWANPAKYGNPNTONNSTNPFVKSTEQKYLTLNTESTRIMT 540  
 QY 541 KLRAGQCRFTWTSFPFKYLEMTGNIDEAEWEMKAGFHRMNNYMMDMKQFNDYTSKESCV 600  
 Db 541 KLRAGQCRFTWTSFPFKYLEMTGNIDEAEWEMKAGFHRMNNYMMDMKQFNDYTSKESCV 600  
 QY 601 GL 602  
 Db 601 GL 602

RESULT 5

ID ABR62392 standard; protein; 602 AA.

AC ABR62392;

DT 03-OCT-2003 (first entry)

DE Human butyrylcholinesterase.

XX Human; butyrylcholinesterase; transgenic; poisoning; antidote; enzyme;

KW EC-3.1.1.8.

OS Homo sapiens.

PH Key Location/Qualifiers

FT Peptide 1..18

FT Protein 19..602

PN W02003054182-A2.

PD 03-JUL-2003.

PF 19-DEC-2002; 2002WO-IB005526.

PR 21-DEC-2001; 2001US-0344295P.

PA (NEXT-) NEXIA BIOTECHNOLOGIES INC.

PI Karatzas C, Huang Y, Lazaris A;

XX WPI; 2003-559148/52.  
 DR N-PSDB; ACC84170.  
 XX New transgenic mammal (e.g. goat) expressing a butyrylcholinesterase  
 PT (BChE) enzyme in its milk or urine, useful for large-scale production of  
 PT recombinant BChE to prevent or treat organophosphate poisoning or cocaine  
 PT intoxication.  
 XX  
 XX Disclousure; Fig 1A; 112pp; English.  
 PS  
 XX The present sequence is the protein sequence of human  
 CC butyrylcholinesterase (BChE), including the native signal peptide which  
 CC is cleaved during processing to produce the mature BChE protein. The  
 CC invention provides methods for large-scale production of recombinant BChE  
 CC in cell culture, and in the milk and/or urine of transgenic mammals. The  
 CC genome of the transgenic mammal (e.g. goat) comprises a DNA sequence that  
 CC encodes BChE operably linked to a mammary gland-specific promoter that  
 CC provides secretion of the BChE enzyme into the milk or urine of the  
 CC mammal. The recombinant BChE can be used in preventing and/or treating  
 CC organophosphate pesticide poisoning, nerve gas poisoning, cocaine  
 CC intoxication or succinylcholine-induced apnoea  
 CC  
 XX  
 SQ Sequence 602 AA;

Query Match 99.4%; Score 3239; DB 6; Length 602;  
 Best Local Similarity 99.7%; Pred. No. 4.3e-287;  
 Matches 600; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDSKVTITICIRFLFWFLLCMLIGKSHTEDDIIATKNGKVRGMNLTVFGTVAFAFGIP 60  
 DB 1 MHSKVTITICIRFLFWFLLCMLIGKSHTEDDIIATKNGKVRGMNLTVFGTVAFAFGIP 60  
 QY 61 YAOPLGLRLFKKQSLTKMSDINWATKYANSCCONIDQSPFGHSEMMNPNTDLSDC 120  
 DB 61 YAOPLGLRLFKKQSLTKMSDINWATKYANSCCONIDQSPFGHSEMMNPNTDLSDC 120  
 QY 121 LYLVNWIIPAKPKKNAATVLIWYGGGFOTGSSLHYVDGKFLARVERIVVSMYRVGALG 180  
 DB 121 LYLVNWIIPAKPKKNAATVLIWYGGGFOTGSSLHYVDGKFLARVERIVVSMYRVGALG 180  
 QY 181 FLALPGNPAFGNMGLEDDQALQWVOXNIAAFGPNKSVTLFGESAGASVSLHLSPG 240  
 DB 181 FLALPGNPAFGNMGLEDDQALQWVOXNIAAFGPNKSVTLFGESAGASVSLHLSPG 240  
 QY 241 SHSLFTRAILQSSGFNAPWAVTSLYEARNRTLAKLTGCSRENTEIILKLRNKDPOEI 300  
 DB 241 SHSLFTRAILQSSGFNAPWAVTSLYEARNRTLAKLTGCSRENTEIILKLRNKDPOEI 300  
 QY 301 LINAFAVVPYGTPLSVNFGPTVDGDFLTDMPDILLELGQFKKTQILVGVNDEBGTAFLLV 360  
 DB 301 LINAFAVVPYGTPLSVNFGPTVDGDFLTDMPDILLELGQFKKTQILVGVNDEBGTAFLLV 360  
 QY 361 GAPFSGKDNNSIITRKEFOEGIKTFFPGVSFEGKESILFHTDWDODRPENYREALGDV 420  
 DB 361 GAPFSGKDNNSIITRKEFOEGIKTFFPGVSFEGKESILFHTDWDODRPENYREALGDV 420  
 QY 421 VGDYNIICPALEFTKKGSEWGNNAFPYYFEHRSSKLPMPEWVGVAHGYEIFVGLPLER 480  
 DB 421 VGDYNIICPALEFTKKGSEWGNNAFPYYFEHRSSKLPMPEWVGVAHGYEIFVGLPLER 480  
 QY 481 RDNTYKAEILSRSLVYKMANFAKGNPNTONNSTSWPVKSTEQKTLTNTSTRTMT 540  
 DB 481 RDNTYKAEILSRSLVYKMANFAKGNPNTONNSTSWPVKSTEQKTLTNTSTRTMT 540  
 QY 541 KLRAGQCRFWTSFPPKYLEMTGNIDEAEMWKAEGFHRNNYMMDMKQNFNDYTSKESCV 600  
 DB 541 KLRAGQCRFWTSFPPKYLEMTGNIDEAEMWKAEGFHRNNYMMDMKQNFNDYTSKESCV 600  
 QY 601 GL 602  
 DB 601 GL 602

RESULT 6  
 ADF90908  
 ID ADF90908 standard; protein; 602 AA.  
 XX  
 XX ADF90908;  
 AC  
 XX

26-FEB-2004 (first entry)

Human hepatic-fibrosis disease marker protein SEQ ID 370.

Hepatic fibrosis; marker; chronic hepatitis; liver cirrhosis;  
 hepatic carcinoma; human.

Homo sapiens.

JP2003259877-A.

16-SEP-2003.

11-MAR-2002; 2002JP-00065013.

11-MAR-2002; 2002JP-00065013.

(SUMU ) SUMITOMO SEIYAKU KK.

WPI; 2003-821598/77.

Hepatic fibrosis disease markers comprising polynucleotides or  
 PT antibodies, useful for improved diagnosis, screening and developing drugs  
 PT to treat hepatitis, for control cirrhosis and carcinoma.  
 XX

Claim 3; SEQ ID NO 370; 313pp; Japanese.

The present invention relates to hepatic-fibrosis disease markers  
 CC (ADP90539-ADP90871) and related proteins (ADP90872-ADP90917). The  
 CC sequences are useful for detecting and treating hepatic fibrosis caused  
 CC by alcohol consumption, virus infection, etc., and the associated chronic  
 CC hepatitis, etc. leading to liver cirrhosis and hepatic carcinoma. The  
 CC markers allow the cause of hepatic fibrosis to be clarified (diagnostic  
 CC precision), so more suitable treatments can be developed and given.  
 CC  
 XX

Sequence 602 AA;

Query Match 99.4%; Score 3239; DB 7; Length 602;  
 Best Local Similarity 99.7%; Pred. No. 4.3e-287;  
 Matches 600; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDSKVTITICIRFLFWFLLCMLIGKSHTEDDIIATKNGKVRGMNLTVFGTVAFAFGIP 60  
 DB 1 MHSKVTITICIRFLFWFLLCMLIGKSHTEDDIIATKNGKVRGMNLTVFGTVAFAFGIP 60  
 QY 61 YAOPLGLRLFKKQSLTKMSDINWATKYANSCCONIDQSPFGHSEMMNPNTDLSDC 120  
 DB 61 YAOPLGLRLFKKQSLTKMSDINWATKYANSCCONIDQSPFGHSEMMNPNTDLSDC 120  
 QY 121 LYLVNWIIPAKPKKNAATVLIWYGGGFOTGSSLHYVDGKFLARVERIVVSMYRVGALG 180  
 DB 121 LYLVNWIIPAKPKKNAATVLIWYGGGFOTGSSLHYVDGKFLARVERIVVSMYRVGALG 180  
 QY 181 FLALPGNPAFGNMGLEDDQALQWVOXNIAAFGPNKSVTLFGESAGASVSLHLSPG 240  
 DB 181 FLALPGNPAFGNMGLEDDQALQWVOXNIAAFGPNKSVTLFGESAGASVSLHLSPG 240  
 QY 241 SHSLFTRAILQSSGFNAPWAVTSLYEARNRTLAKLTGCSRENTEIILKLRNKDPOEI 300  
 DB 241 SHSLFTRAILQSSGFNAPWAVTSLYEARNRTLAKLTGCSRENTEIILKLRNKDPOEI 300  
 QY 301 LINAFAVVPYGTPLSVNFGPTVDGDFLTDMPDILLELGQFKKTQILVGVNDEBGTAFLLV 360  
 DB 301 LINAFAVVPYGTPLSVNFGPTVDGDFLTDMPDILLELGQFKKTQILVGVNDEBGTAFLLV 360

QY 361 GAFGFSKDNNSITTRKEFOGGLKIFPPGVSEFGKESILFHYYTDMVDDQRENYREALGV 420  
 DB 361 GAFGFSKDNNSITTRKEFOGGLKIFPPGVSEFGKESILFHYYTDMVDDQRENYREALGV 420  
 QY 421 VGDYNTFCPLAEFTKFSSEWGNNAFFYYFEHRSKILPPEMGMVHGYEIEFVGLPLER 480  
 DB 421 VGDYNTFCPLAEFTKFSSEWGNNAFFYYFEHRSKILPPEMGMVHGYEIEFVGLPLER 480  
 QY 481 RDNVTKAEILSRISIVKRWANPAKYGNPNETONNSTSWPVFKSTEOKYTLTNTSTRIMT 540  
 DB 481 RDNVTKAEILSRISIVKRWANPAKYGNPNETONNSTSWPVFKSTEOKYTLTNTSTRIMT 540  
 QY 541 KLRAGQCRFWTSFPPKYLEMTGNIDBAEWKAGFHRNNYMMDMKQPNFYTSKESCV 600  
 DB 541 KLRAGQCRFWTSFPPKYLEMTGNIDBAEWKAGFHRNNYMMDMKQPNFYTSKESCV 600  
 QY 601 GL 602  
 DB 601 GL 602

## RESULT 7

AA44574 ID AA44574 standard; protein; 602 AA.

AA44574;

04-APR-2000 (first entry)

Human Butyrylcholinesterase-K (BCH-E-K) protein.

Butyrylcholinesterase-K; BCH-E-K; BCH-E allele; neurological disease;  
 therapy; treatment; allelic variant; apoB4 allele; neurofibromatosis;  
 non-AD neurological disease; Alzheimer's disease; Huntington's disease;  
 depression; amyotrophic lateral sclerosis; multiple sclerosis; stroke;  
 Parkinson's disease; multi-infarct dementia; human.

Homo sapiens.

Key Location/Qualifiers

Misc-difference 567 /note="wild type Ala replaced with Thr"

MO996072-A2.

23-DEC-1999.

16-JUN-1999; 99WO-IB001298.

16-JUN-1998; 98US-0089406P.

(NOVA-) NOVA MOLECULAR INC.

Sevigny P, Wiebusch H, Schappert K;

WPI; 2000-126550/11.

N-PSDB; AA249471.

Prediction of drug efficacy for treating neurological diseases like

Alzheimer's disease, neurofibromatosis, Huntington's disease.

Disclosure; Fig 4; 37p; English.

The present sequence is the human polymorphic variant  
 butyrylcholinesterase-K (BCH-E-K) protein. BCH-E-K is an allelic variant of  
 BCH-E. Determining BCH-E allele status (homozygous or heterozygous) of a  
 patient helps predicting risk of neurological diseases, efficacy of a  
 therapy and determining treatment protocol. BCH-E-K and apoB4 allele  
 status also indicate patient's risk for having a neurological disease.  
 This method enables treating Alzheimer's disease, Huntington's disease,  
 depression, neurofibromatosis, amyotrophic lateral sclerosis, stroke,  
 multiple sclerosis, Parkinson's disease, multi-infarct dementia and other  
 non-AD neurological diseases

XX Sequence 602 AA;

Query Match 99.2%; Score 3235; DB 3; Length 602;  
 Best Local Similarity 99.5%; Pred. No. 1e-286;  
 Matches 599; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MDSKVTIICIRLFNFWLLCMILGKSHTEDDIIITKNGKRGKMLTVFGTVAFLGIP 60  
 DB 1 MDSKVTIICIRLFNFWLLCMILGKSHTEDDIIITKNGKRGKMLTVFGTVAFLGIP 60  
 QY 61 YVQPLGLRLFRKQPSGLTWSDIWNATKXANCCNINQSPFGFSGSEMMNNTLSDC 120  
 DB 61 YVQPLGLRLFRKQPSGLTWSDIWNATKXANCCNINQSPFGFSGSEMMNNTLSDC 120  
 QY 121 LYINWMI PAPKPKNTVLIMWYGGFQGTSLAHYDGFKLARVERVIVSNMYRVALG 180  
 DB 121 LYINWMI PAPKPKNTVLIMWYGGFQGTSLAHYDGFKLARVERVIVSNMYRVALG 180  
 QY 181 FLALPGRNPEAPGNMGLFDQQLALQWYQKIIAAGGNPKSVTLFGESAGAAVSJHLSPG 240  
 DB 181 FLALPGRNPEAPGNMGLFDQQLALQWYQKIIAAGGNPKSVTLFGESAGAAVSJHLSPG 240  
 QY 241 SHSLFTFRLILQSGSFNAPWAVTSIYEARRTINLAKLGCSSENETEIIKCLRNDPOBI 300  
 DB 241 SHSLFTFRLILQSGSFNAPWAVTSIYEARRTINLAKLGCSSENETEIIKCLRNDPOBI 300  
 QY 301 LINEAFVVEYGTPLSVNFGPTVDGDFLTDMPDILLELQGFKKTQILVGNKDEGTWFLVY 360  
 DB 301 LINEAFVVEYGTPLSVNFGPTVDGDFLTDMPDILLELQGFKKTQILVGNKDEGTWFLVY 360  
 QY 361 GAFGFSKDNNSITTRKEFOGGLKIFPPGVSEFGKESILFHYYTDMVDDQRENYREALGV 420  
 DB 361 GAFGFSKDNNSITTRKEFOGGLKIFPPGVSEFGKESILFHYYTDMVDDQRENYREALGV 420  
 QY 421 VGDYNTFCPLAEFTKFSSEWGNNAFFYYFEHRSKILPPEMGMVHGYEIEFVGLPLER 480  
 DB 421 VGDYNTFCPLAEFTKFSSEWGNNAFFYYFEHRSKILPPEMGMVHGYEIEFVGLPLER 480  
 QY 481 RDNVTKAEILSRISIVKRWANPAKYGNPNETONNSTSWPVFKSTEOKYTLTNTSTRIMT 540  
 DB 481 RDNVTKAEILSRISIVKRWANPAKYGNPNETONNSTSWPVFKSTEOKYTLTNTSTRIMT 540  
 QY 541 KLRAGQCRFWTSFPPKYLEMTGNIDBAEWKAGFHRNNYMMDMKQPNFYTSKESCV 600  
 DB 541 KLRAGQCRFWTSFPPKYLEMTGNIDBAEWKAGFHRNNYMMDMKQPNFYTSKESCV 600  
 QY 601 GL 602  
 DB 601 GL 602

## RESULT 8

AA49483 ID AA49483 standard; protein; 602 AA.

AA49483;

27-MAR-2000 (first entry)

Human butyryl cholinesterase (BuChE) mutant.

Organophosphate; detoxification; esterase; acetylcholinesterase; AChE;  
 butyrylcholinesterase; BuChE; carboxylesterase; CaE; sheep dip; human;  
 nerve agent; organophosphorus acid anhydride; OPAA; mutant.

Homo sapiens.

Synthetic.

US6001625-A.

14-DEC-1999.





CC human cholinesterase, was used as a probe to obtain the full-length  
CC pseudocholinesterase sequence (AA042496). (Updated on 25-MAR-2003 to  
CC correct PF field.)

XX Sequence 602 AA;

Query Match 99.2%; Score 3233; DB 2; Length 602;

Best Local Similarity 99.5%; Pred. No. 1.5e-286; Indels 0; Gaps 0;

Matches 599; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 1 MDSKVTIIICIRPLFWFLLCMLIGKSHTEDDIIATKNGKRGKNTLVFGTVAFLGIP 60
DB 1 MHSKVTIIICIRPLFWFLLCMLIGKSHTEDDIIATKNGKRGKNTLVFGTVAFLGIP 60
QY 61 YAOPLGRLEPKKQSLTKMSDIWNAKYANSCCONIDQSPGHSEMMNPNTDISEDC 120
DB 61 YAOPLGRLEPKKQSLTKMSDIWNAKYANSCCONIDQSPGHSEMMNPNTDISEDC 120
QY 121 LYLNWMIAPKPKNAATVLIWYGGGFOTGTSLSHVDGKFLARVERIVVMYRYGALG 180
DB 121 LYLNWMIAPKPKNAATVLIWYGGGFOTGTSLSHVDGKFLARVERIVVMYRYGALG 180
QY 181 FLALPGNPEAPGNMGLFDQDLALQWQKNTAAGGNPKSVTLFGESAGAAVSLLHLSPG 240
DB 181 FLALPGNPEAPGNMGLFDQDLALQWQKNTAAGGNPKSVTLFGESAGAAVSLLHLSPG 240
QY 241 SHSLFTRAIIQSGSFNAPMAVTSLEYARNRTLNALKTGCSRENETEIIKCLRNKDOEI 300
DB 241 SHSLFTRAIIQSGSFNAPMAVTSLEYARNRTLNALKTGCSRENETEIIKCLRNKDOEI 300
QY 301 LLINEAFVVPYGTPLSVNFGPTVDGFLTMDPDLLELGOFPKQTQILVGNKDEGTWFLVY 360
DB 301 LLINEAFVVPYGTPLSVNFGPTVDGFLTMDPDLLELGOFPKQTQILVGNKDEGTWFLVY 360
QY 361 GADPFSKDNNSITTRKEFOEGKIFPPGVSEFKESILFHYTDWDDQRPENYREALGDV 420
DB 361 GADPFSKDNNSITTRKEFOEGKIFPPGVSEFKESILFHYTDWDDQRPENYREALGDV 420
QY 421 VGDYNIICPALLETFFKSEWGNNAFFYYFEHRSSKLPWPEMGMVHGYEIEFVFGPLER 480
DB 421 VGDYNIICPALLETFFKSEWGNNAFFYYFEHRSSKLPWPEMGMVHGYEIEFVFGPLER 480
QY 481 RDNYTKAEILSRISIVRWANFAKYGNPNETONNSTWPKSTEQKYLTLNTESTRIMT 540
DB 481 RDNYTKAEILSRISIVRWANFAKYGNPNETONNSTWPKSTEQKYLTLNTESTRIMT 540
QY 541 KLRAGOCRFMTSFPKYLEMTGNIDEABEWKAGFHRMNNYMDKNQFNDYTSKESCV 600
DB 541 KLRAGOCRFMTSFPKYLEMTGNIDEABEWKAGFHRMNNYMDKNQFNDYTSKESCV 600
QY 601 GL 602
DB 601 GL 602

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RESULT 10

AAV49474 ID AAV49474 standard; protein; 602 AA.

XX AAV49474;

DT 27-MAR-2000 (first entry)

DE Human butyryl cholinesterase (BuChE) mutant.

XX Organophosphate; detoxification; esterase; acetylcholinesterase; AChE;

KM butyrylcholinesterase; BuChE; carboxylesterase; Car; sheep dip; human;

XX nerve agent; organophosphorus acid anhydride; OPAA; mutant.

OS Homo sapiens.

XX Synthetic.

PN US6001625-A.

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XX 14-DEC-1999.
PD 19-MAY-1995; 95US-00446100.
XX 19-MAY-1995; 95US-00446100.
XX 19-MAY-1995; 95US-00446100.
XX (USSA ) US SEC OF ARMY.
PA Broomfield CA, Lockridge O, Millard CB;
PI WPI; 2000-096137/08.
PT Enhancing the organophosphate detoxifying capabilities of esterases for
PT the treatment of organophosphate poisoning.
PS Disclosure; Col 3-6; 64pp; English.
XX The invention provides a method of enhancing organophosphate detoxifying
CC capabilities of esterases (either human acetylcholinesterases (AChE), that
CC human butyrylcholinesterases (BuChE) and/or carboxylesterases (Car)), that
CC comprises substituting a histidine residue for 1 or more amino acid(s)
CC within 6 Angstrom of an active site serine. The method may be used for
CC enhancing organophosphate detoxifying capabilities of esterases (either
CC human AChE, human BuChE and/or human Car). The modified esterases may
CC then be used to treat agricultural workers poisoned with organophosphates
CC through contact with chemical such as sheep dips. They may also be used
CC to treat military personnel contaminated by chemical weaponry such as
CC nerve agents. Additionally, the esterases may also be used to
CC decontaminate ground and buildings and equipment used to store, or
CC contaminated by organophosphates. The method produces esterases with
CC improved detoxification properties over naturally occurring
CC organophosphorus acid anhydride (OPAA) hydrolyzing enzymes. They are also
CC less likely to be inactivated by the OPAA
XX
SQ Sequence 602 AA;
Query Match 99.1%; Score 3232; DB 3; Length 602;
Best Local Similarity 99.5%; Pred. No. 1.9e-286; Indels 0; Gaps 0;
Matches 599; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 MDSKVTIIICIRPLFWFLLCMLIGKSHTEDDIIATKNGKRGKNTLVFGTVAFLGIP 60
DB 1 MHSKVTIIICIRPLFWFLLCMLIGKSHTEDDIIATKNGKRGKNTLVFGTVAFLGIP 60
QY 61 YAOPLGRLEPKKQSLTKMSDIWNAKYANSCCONIDQSPGHSEMMNPNTDISEDC 120
DB 61 YAOPLGRLEPKKQSLTKMSDIWNAKYANSCCONIDQSPGHSEMMNPNTDISEDC 120
QY 121 LYLNWMIAPKPKNAATVLIWYGGGFOTGTSLSHVDGKFLARVERIVVMYRYGALG 180
DB 121 LYLNWMIAPKPKNAATVLIWYGGGFOTGTSLSHVDGKFLARVERIVVMYRYGALG 180
QY 181 FLALPGNPEAPGNMGLFDQDLALQWQKNTAAGGNPKSVTLFGESAGAAVSLLHLSPG 240
DB 181 FLALPGNPEAPGNMGLFDQDLALQWQKNTAAGGNPKSVTLFGESAGAAVSLLHLSPG 240
QY 241 SHSLFTRAIIQSGSFNAPMAVTSLEYARNRTLNALKTGCSRENETEIIKCLRNKDOEI 300
DB 241 SHSLFTRAIIQSGSFNAPMAVTSLEYARNRTLNALKTGCSRENETEIIKCLRNKDOEI 300
QY 301 LLINEAFVVPYGTPLSVNFGPTVDGFLTMDPDLLELGOFPKQTQILVGNKDEGTWFLVY 360
DB 301 LLINEAFVVPYGTPLSVNFGPTVDGFLTMDPDLLELGOFPKQTQILVGNKDEGTWFLVY 360
QY 361 GADPFSKDNNSITTRKEFOEGKIFPPGVSEFKESILFHYTDWDDQRPENYREALGDV 420
DB 361 GADPFSKDNNSITTRKEFOEGKIFPPGVSEFKESILFHYTDWDDQRPENYREALGDV 420
QY 421 VGDYNIICPALLETFFKSEWGNNAFFYYFEHRSSKLPWPEMGMVHGYEIEFVFGPLER 480
DB 421 VGDYNIICPALLETFFKSEWGNNAFFYYFEHRSSKLPWPEMGMVHGYEIEFVFGPLER 480

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QY 481 RDNTYKAEILLSRSIVKMANFAKYNPNETONNSTSWPVFKSTEQKYLTLNTESTRIMT 540  
 DB 481 RDNTYKAEILLSRSIVKMANFAKYNPNETONNSTSWPVFKSTEQKYLTLNTESTRIMT 540  
 QY 541 KLRQQCRFWTSFPPKYLEMTGNIDEAEWEMKAGFHRMNNYMDWKQFNDYTSKESCV 600  
 DB 541 KLRQQCRFWTSFPPKYLEMTGNIDEAEWEMKAGFHRMNNYMDWKQFNDYTSKESCV 600  
 QY 601 GL 602  
 DB 601 GL 602  
 RESULT 11  
 ID AAY49473 standard; protein; 602 AA.  
 AC AAY49473;  
 DT 27-MAR-2000 (first entry)  
 XX Human butyryl cholinesterase (BuChE) mutant.  
 DE Organophosphate; detoxification; esterase; acetylcholinesterase; AChE;  
 KW butyrylcholinesterase; BuChE; carboxylesterase; CaB; sheep dip; human;  
 KM nerve agent; organophosphorus acid anhydride; OPAA; mutant.  
 OS Homo sapiens.  
 OS Synthetic.  
 PN US6001625-A.  
 PD 14-DEC-1999.  
 XX 19-MAY-1995; 95US-00446100.  
 PR 19-MAY-1995; 95US-00446100.  
 PA (USSA ) US SEC OF ARMY.  
 FI Broomfield CA, Lockridge O, Millard CB;  
 XX WPI; 2000-096137/08.  
 PT Enhancing the organophosphate detoxifying capabilities of esterases for  
 the treatment of organophosphate poisoning.  
 PS Disclosure; Col 3-4; 64pp; English.  
 XX The invention provides a method of enhancing organophosphate detoxifying  
 CC capabilities of esterases (either human acetylcholinesterases (AChE), that  
 CC human butyrylcholinesterases (BuChE) and/or carboxylesterases (CaB)), that  
 CC comprises substituting a histidine residue for I or more amino acid(s)  
 CC within 6 Angstrom of an active site serine. The method may be used for  
 CC enhancing organophosphate detoxifying capabilities of esterases (either  
 CC human AChE, human BuChE and/or human CaB). The modified esterases may  
 CC then be used to treat agricultural workers poisoned with organophosphates  
 CC through contact with chemical such as sheep dips. They may also be used  
 CC to treat military personnel contaminated by chemical weapons such as  
 CC nerve agents. Additionally, the esterases may also be used to  
 CC decontaminate ground and buildings and equipment used to store, or  
 CC contaminated by organophosphates. The method produces esterases with  
 CC improved detoxification properties over naturally occurring  
 CC organophosphorus acid anhydride (OPAA) hydrolyzing enzymes. They are also  
 CC less likely to be inactivated by the OPAA  
 SQ Sequence 602 AA;  
 Query Match 99.1%; Score 3232; DB 3; Length 602;  
 Best Local Similarity 99.5%; Pred. No. 1.9e-286;  
 Matches 599; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 MDSKVTITICRFLFWPILLCLMLIGKSHTEDDIIATKNGKVRGNLTVFGTVAFAFGIP 60

DB 1 MDSKVTITICRFLFWPILLCLMLIGKSHTEDDIIATKNGKVRGNLTVFGTVAFAFGIP 60  
 QY 61 YAOPLGRLEAFKPKPOSTLTKMSDIWNAATKYNSSCONIDJSPGPHGSEMMNPNTDLSBDC 120  
 DB 61 YAOPLGRLEAFKPKPOSTLTKMSDIWNAATKYNSSCONIDJSPGPHGSEMMNPNTDLSBDC 120  
 QY 121 LYNWMIAPKPKRNATVLWIVGGGFGTGSLSHVYDGKFLAVERVIVSMYRVGALG 180  
 DB 121 LYNWMIAPKPKRNATVLWIVGGGFGTGSLSHVYDGKFLAVERVIVSMYRVGALG 180  
 QY 181 FLALPGNBPARGWGLFDQOLALQWOKNTAARGNPKSTYLLGESGAASVSLHLSPG 240  
 DB 181 FLALPGNBPARGWGLFDQOLALQWOKNTAARGNPKSTYLLGESGAASVSLHLSPG 240  
 QY 241 SHSLFTRAILQSGSFNAPMAVTSLYEARNRTLMLAKLTGCSRENETIILCLRKQDPEI 300  
 DB 241 SHSLFTRAILQSGSFNAPMAVTSLYEARNRTLMLAKLTGCSRENETIILCLRKQDPEI 300  
 QY 301 LLINEAFVVPYGTPLSVNFGFTVDGDLTDMPDILLLEIGQFKKQIILGVNKGDEGTWFLVY 360  
 DB 301 LLINEAFVVPYGTPLSVNFGFTVDGDLTDMPDILLLEIGQFKKQIILGVNKGDEGTWFLVY 360  
 QY 361 GARGFSKDNNSITTRKEFGGLKIFPPGVSEFGKESILFHYTWDVDDQRENTREALGDV 420  
 DB 361 GARGFSKDNNSITTRKEFGGLKIFPPGVSEFGKESILFHYTWDVDDQRENTREALGDV 420  
 QY 421 VGDVNFICPALFETKRSSEWGNNAFFYFPEHRSKLPMPBMGMVGHYELEFPVGLER 480  
 DB 421 VGDVNFICPALFETKRSSEWGNNAFFYFPEHRSKLPMPBMGMVGHYELEFPVGLER 480  
 QY 481 RDNTYKAEILLSRSIVKMANFAKYNPNETONNSTSWPVFKSTEQKYLTLNTESTRIMT 540  
 DB 481 RDNTYKAEILLSRSIVKMANFAKYNPNETONNSTSWPVFKSTEQKYLTLNTESTRIMT 540  
 QY 541 KLRQQCRFWTSFPPKYLEMTGNIDEAEWEMKAGFHRMNNYMDWKQFNDYTSKESCV 600  
 DB 541 KLRQQCRFWTSFPPKYLEMTGNIDEAEWEMKAGFHRMNNYMDWKQFNDYTSKESCV 600  
 QY 601 GL 602  
 DB 601 GL 602  
 RESULT 12  
 ID AAY49475 standard; protein; 602 AA.  
 AC AAY49475;  
 DT 27-MAR-2000 (first entry)  
 XX Human butyryl cholinesterase (BuChE) mutant.  
 DE Organophosphate; detoxification; esterase; acetylcholinesterase; AChE;  
 KW butyrylcholinesterase; BuChE; carboxylesterase; CaB; sheep dip; human;  
 KM nerve agent; organophosphorus acid anhydride; OPAA; mutant.  
 OS Homo sapiens.  
 OS Synthetic.  
 PN US6001625-A.  
 PD 14-DEC-1999.  
 XX 19-MAY-1995; 95US-00446100.  
 PR 19-MAY-1995; 95US-00446100.  
 PA (USSA ) US SEC OF ARMY.  
 FI Broomfield CA, Lockridge O, Millard CB;  
 XX

DR WPI; 2000-096137/08.  
 XX Enhancing the organophosphate detoxifying capabilities of esterases for  
 PT the treatment of organophosphate poisoning.  
 XX  
 PS Disclosure; Col 5-6; 64pp; English.  
 XX  
 CC The invention provides a method of enhancing organophosphate detoxifying  
 CC capabilities of esterases (either human acetylcholinesterases (AChE), that  
 CC human butyrylcholinesterases (BuChE) and/or carboxylesterases (CaE)), that  
 CC comprises substituting a histidine residue for 1 or more amino acid(s)  
 CC within 6 Angstrom of an active site serine. The method may be used for  
 CC enhancing organophosphate detoxifying capabilities of esterases (either  
 CC human AChE, human BuChE and/or human CaE). The modified esterases may  
 CC then be used to treat agricultural workers poisoned with organophosphates  
 CC through contact with chemical such as sheep dips. They may also be used  
 CC to treat military personnel contaminated by chemical weaponry such as  
 CC nerve agents. Additionally, the esterases may also be used to  
 CC decontaminate ground and buildings and equipment used to store, or  
 CC contaminated by organophosphates. The method produces esterases with  
 CC improved detoxification properties over naturally occurring  
 CC organophosphorus acid anhydride (OPAA) hydrolyzing enzymes. They are also  
 CC less likely to be inactivated by the OPAA  
 XX  
 SQ Sequence 602 AA:  
 Query Match 99.1%; Score 3232; DB 3; Length 602;  
 Best Local Similarity 99.5%; Pred. No. 1.9e-286;  
 Matches 599; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 MDSKTTTICIRFLFWFLLCMLIGKSHTEDDIIATKNGKVRGMNLTVFGTVAFAFGIP 60  
 DB 1 MHSKVTITICIRFLFWFLLCMLIGKSHTEDDIIATKNGKVRGMNLTVFGTVAFAFGIP 60  
 QY 61 YAQPLGLRLFRFKKQSLTKMSDIMNATKYANSCCONIDQSPFGHSEMMNPNTDLSDC 120  
 DB 61 YAQPLGLRLFRFKKQSLTKMSDIMNATKYANSCCONIDQSPFGHSEMMNPNTDLSDC 120  
 QY 121 LYANWMIAPRKPKNATVLIWYGGGFORGTSSLIHYDGKFLARERVLVSMNTRVGLG 180  
 DB 121 LYANWMIAPRKPKNATVLIWYGGGFORGTSSLIHYDGKFLARERVLVSMNTRVGLG 180  
 QY 121 LYANWMIAPRKPKNATVLIWYGGGFORGTSSLIHYDGKFLARERVLVSMNTRVGLG 180  
 DB 121 LYANWMIAPRKPKNATVLIWYGGGFORGTSSLIHYDGKFLARERVLVSMNTRVGLG 180  
 QY 181 FLALPGNPEAPGNMGLPQOLALQWQKIAAFGNPKSVTLFGESAGASVSLHLSPG 240  
 DB 181 FLALPGNPEAPGNMGLPQOLALQWQKIAAFGNPKSVTLFGESAGASVSLHLSPG 240  
 QY 181 FLALPGNPEAPGNMGLPQOLALQWQKIAAFGNPKSVTLFGESAGASVSLHLSPG 240  
 DB 181 FLALPGNPEAPGNMGLPQOLALQWQKIAAFGNPKSVTLFGESAGASVSLHLSPG 240  
 QY 241 SHSLFTRAILQSGSFNAFWAVTSIYEARNRITLAKLTGCSRENTEIILKLRNKDPOEI 300  
 DB 241 SHSLFTRAILQSGSFNAFWAVTSIYEARNRITLAKLTGCSRENTEIILKLRNKDPOEI 300  
 QY 241 SHSLFTRAILQSGSFNAFWAVTSIYEARNRITLAKLTGCSRENTEIILKLRNKDPOEI 300  
 DB 241 SHSLFTRAILQSGSFNAFWAVTSIYEARNRITLAKLTGCSRENTEIILKLRNKDPOEI 300  
 QY 301 LLNENFVVPYGTPLSVNFGPVDGDELMDPILILEGPKKTOILVGNKDEGTWFLVY 360  
 DB 301 LLNENFVVPYGTPLSVNFGPVDGDELMDPILILEGPKKTOILVGNKDEGTWFLVY 360  
 QY 301 LLNENFVVPYGTPLSVNFGPVDGDELMDPILILEGPKKTOILVGNKDEGTWFLVY 360  
 DB 301 LLNENFVVPYGTPLSVNFGPVDGDELMDPILILEGPKKTOILVGNKDEGTWFLVY 360  
 QY 361 GAPGSKDNNSIITTKRFOEGIKIFPPGVSEFGKESILFHYTDWVDORPENYRRLADGV 420  
 DB 361 GAPGSKDNNSIITTKRFOEGIKIFPPGVSEFGKESILFHYTDWVDORPENYRRLADGV 420  
 QY 421 VGDYNPICPALFTTKKFSFEMGNNAFFYFERRSSKLPEPMWGMHGEIEBVFCLPLER 480  
 DB 421 VGDYNPICPALFTTKKFSFEMGNNAFFYFERRSSKLPEPMWGMHGEIEBVFCLPLER 480  
 QY 481 RNNYKABEILRSIYKRWANPAKGNPETONNSSTWPFSTOKLTLNTESSTRIMT 540  
 DB 481 RNNYKABEILRSIYKRWANPAKGNPETONNSSTWPFSTOKLTLNTESSTRIMT 540  
 QY 541 KLRACQCRFTWTSFFPVLEMTGNIDAEWEMKAGFHRNNNMMDKNOFNDYTSKESCV 600  
 DB 541 KLRACQCRFTWTSFFPVLEMTGNIDAEWEMKAGFHRNNNMMDKNOFNDYTSKESCV 600  
 QY 601 GL 602  
 DB 601 GL 602  
 QY 601 GL 602  
 DB 601 GL 602

RESULT 13  
 AA49472  
 ID AA49472 standard; protein; 602 AA.  
 XX  
 AC AA49472;  
 XX  
 DT 27-MAR-2000 (first entry)  
 XX  
 DE Human butyryl cholinesterase (BuChE) mutant G117H.  
 XX  
 KM Organophosphate; detoxification; esterase; acetylcholinesterase; AChE;  
 KM butyrylcholinesterase; BuChE; carboxylesterase; CaE; sheep dip; human;  
 KM nerve agent; organophosphorus acid anhydride; OPAA; mutant.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 FH Key Location/Qualifiers  
 FT Misc-difference 145 /note="wild-type Gly is replaced with His"  
 FT  
 XX US6001625-A.  
 XX  
 XX 14-DEC-1999.  
 XX  
 XX 19-MAY-1995; 95US-00446100.  
 XX  
 XX 19-MAY-1995; 95US-00446100.  
 XX  
 XX (US5A ) US SEC OF ARMY.  
 XX  
 XX Broomfield CA, Lockridge O, Millard CB;  
 XX  
 XX WPI; 2000-096137/08.  
 XX  
 PT Enhancing the organophosphate detoxifying capabilities of esterases for  
 PT the treatment of organophosphate poisoning.  
 XX  
 PS Claim 10; Col 123-126; 64pp; English.  
 XX  
 CC The invention provides a method of enhancing organophosphate detoxifying  
 CC capabilities of esterases (either human acetylcholinesterases (AChE), that  
 CC human butyrylcholinesterases (BuChE) and/or carboxylesterases (CaE)), that  
 CC comprises substituting a histidine residue for 1 or more amino acid(s)  
 CC within 6 Angstrom of an active site serine. The method may be used for  
 CC enhancing organophosphate detoxifying capabilities of esterases (either  
 CC human AChE, human BuChE and/or human CaE). The modified esterases may  
 CC then be used to treat agricultural workers poisoned with organophosphates  
 CC through contact with chemical such as sheep dips. They may also be used  
 CC to treat military personnel contaminated by chemical weaponry such as  
 CC nerve agents. Additionally, the esterases may also be used to  
 CC decontaminate ground and buildings and equipment used to store, or  
 CC contaminated by organophosphates. The method produces esterases with  
 CC improved detoxification properties over naturally occurring  
 CC organophosphorus acid anhydride (OPAA) hydrolyzing enzymes. They are also  
 CC less likely to be inactivated by the OPAA  
 XX  
 SQ Sequence 602 AA:  
 Query Match 99.1%; Score 3231; DB 3; Length 602;  
 Best Local Similarity 99.5%; Pred. No. 2.3e-286;  
 Matches 599; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 MDSKTTTICIRFLFWFLLCMLIGKSHTEDDIIATKNGKVRGMNLTVFGTVAFAFGIP 60  
 DB 1 MHSKVTITICIRFLFWFLLCMLIGKSHTEDDIIATKNGKVRGMNLTVFGTVAFAFGIP 60  
 QY 61 YAQPLGLRLFRFKKQSLTKMSDIMNATKYANSCCONIDQSPFGHSEMMNPNTDLSDC 120  
 DB 61 YAQPLGLRLFRFKKQSLTKMSDIMNATKYANSCCONIDQSPFGHSEMMNPNTDLSDC 120

QY 121 LYNWMIIPAKPKNAATVLIWYGGGFQGTSSLHVYDGKFLARVERVIIVSMNTRVAGLG 180  
 Db 121 LYNWMIIPAKPKNAATVLIWYGGGFQGTSSLHVYDGKFLARVERVIIVSMNTRVAGLG 180  
 QY 181 FLALPGNPEAPGNMGLFDQOLALQWOKNTAAFGNPKSVTLFGESAGASVSLHLSPG 240  
 Db 181 FLALPGNPEAPGNMGLFDQOLALQWOKNTAAFGNPKSVTLFGESAGASVSLHLSPG 240  
 QY 241 SHSLFTRAIIQSOSFNAPMAVTSLEYEARNTLAKLTGCSRENEMETIICKLRKDPQEI 300  
 Db 241 SHSLFTRAIIQSOSFNAPMAVTSLEYEARNTLAKLTGCSRENEMETIICKLRKDPQEI 300  
 QY 301 LNEAFVVPYGTPLSVNFGPTVDGFLTDMPDILLELQFCKTQIIVGVNKBEGTWFLVY 360  
 Db 301 LNEAFVVPYGTPLSVNFGPTVDGFLTDMPDILLELQFCKTQIIVGVNKBEGTWFLVY 360  
 QY 361 GABGFSKDNNSITTRKEFQEGKIFPPGVSEFGKESILFHYTDWVDDQRPENYREALGDV 420  
 Db 361 GABGFSKDNNSITTRKEFQEGKIFPPGVSEFGKESILFHYTDWVDDQRPENYREALGDV 420  
 QY 421 VGDYNFICPALFETKTSSEWGNNAFFYYFHRSSKLPMPBMGMVHGIELEFVGLPLER 480  
 Db 421 VGDYNFICPALFETKTSSEWGNNAFFYYFHRSSKLPMPBMGMVHGIELEFVGLPLER 480  
 QY 481 RDNYTKAEIILSRISIVKMANPAKYGNPNETONNSTSWPVKSTEOKYLTLNTESTRIMT 540  
 Db 481 RDNYTKAEIILSRISIVKMANPAKYGNPNETONNSTSWPVKSTEOKYLTLNTESTRIMT 540  
 QY 541 KLRAGQCRFWTSFPPKYLEMTGNIDEAEWEKAGFHRMNNYMDMKNQFNDYTSKESCV 600  
 Db 541 KLRAGQCRFWTSFPPKYLEMTGNIDEAEWEKAGFHRMNNYMDMKNQFNDYTSKESCV 600  
 QY 601 GL 602  
 Db 601 GL 602

RESULT 14

AAV49476  
 ID AAV49476 standard; protein; 602 AA.

AC AAV49476;  
 DT 27-MAR-2000 (first entry)  
 XX Human butyryl cholinesterase (BuChE) mutant.  
 XX Organophosphate; detoxification; esterase; acetylcholinesterase; AChE;  
 KM butyrylcholinesterase; BuChE; carboxylesterase; CaB; sheep dip; human;  
 KM nerve agent; organophosphorus acid anhydride; OPA; mutant.  
 XX Homo sapiens.  
 OS Synthetic.  
 XX US6001625-A.  
 PN 14-DEC-1999.  
 PD 14-DEC-1999.  
 XX 19-MAY-1995; 95US-00446100.  
 PR 19-MAY-1995; 95US-00446100.  
 XX (USSA ) US SEC OF ARMY.  
 PA Broomfield CA, Lockridge O, Millard CB;  
 XX WPI; 2000-096137/08.  
 XX Enhancing the organophosphate detoxifying capabilities of esterases for  
 PT the treatment of organophosphate poisoning.  
 XX Disclosure; Col 5-6; 64pp; English.

CC The invention provides a method of enhancing organophosphate detoxifying  
 CC capabilities of esterases (either human acetylcholinesterases (AChE),  
 CC human butyrylcholinesterases (BuChE) and/or carboxylesterases (CaB)), that  
 CC comprises substituting a histidine residue for 1 or more amino acid(s)  
 CC within 6 Angstrom of an active site serine. The method may be used for  
 CC enhancing organophosphate detoxifying capabilities of esterases (either  
 CC human AChE, human BuChE and/or human CaB). The modified esterases may  
 CC then be used to treat agricultural workers poisoned with organophosphates  
 CC through contact with chemical such as sheep dips. They may also be used  
 CC to treat military personnel contaminated by chemical weaponry such as  
 CC nerve agents. Additionally, the esterases may also be used to  
 CC decontaminate ground and buildings and equipment used to store, or  
 CC contaminated by organophosphates. The method produces esterases with  
 CC improved detoxification properties over naturally occurring  
 CC organophosphorus acid anhydride (OPA) hydrolyzing enzymes. They are also  
 CC less likely to be inactivated by the OPA  
 XX Sequence 602 AA;  
 SQ

Query Match 99.1%; Score 3231; DB 3; Length 602;  
 Best Local Similarity 99.5%; Pred. No. 2,3e-286;  
 Matches 599; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MDSKVITICIRPLFWILLCLIGKSHTEBDIIATKNGKVRGMNLTVEGCTYAFIGIP 60  
 Db 1 MHSKVITICIRPLFWILLCLIGKSHTEBDIIATNGKVRGMNLTVEGCTYAFIGIP 60  
 QY 61 YAOPLGRLEFPKPOSITTKMSDIWNAATKYANSCCONIDQSPFGHSEMMNPNTDSEDC 120  
 Db 61 YAOPLGRLEFPKPOSITTKMSDIWNAATKYANSCCONIDQSPFGHSEMMNPNTDSEDC 120  
 QY 121 LYNWMIIPAKPKNAATVLIWYGGGFQGTSSLHVYDGKFLARVERVIIVSMNTRVAGLG 180  
 Db 121 LYNWMIIPAKPKNAATVLIWYGGGFQGTSSLHVYDGKFLARVERVIIVSMNTRVAGLG 180  
 QY 181 FLALPGNPEAPGNMGLFDQOLALQWOKNTAAFGNPKSVTLFGESAGASVSLHLSPG 240  
 Db 181 FLALPGNPEAPGNMGLFDQOLALQWOKNTAAFGNPKSVTLFGESAGASVSLHLSPG 240  
 QY 241 SHSLFTRAIIQSOSFNAPMAVTSLEYEARNTLAKLTGCSRENEMETIICKLRKDPQEI 300  
 Db 241 SHSLFTRAIIQSOSFNAPMAVTSLEYEARNTLAKLTGCSRENEMETIICKLRKDPQEI 300  
 QY 301 LNEAFVVPYGTPLSVNFGPTVDGFLTDMPDILLELQFCKTQIIVGVNKBEGTWFLVY 360  
 Db 301 LNEAFVVPYGTPLSVNFGPTVDGFLTDMPDILLELQFCKTQIIVGVNKBEGTWFLVY 360  
 QY 361 GABGFSKDNNSITTRKEFQEGKIFPPGVSEFGKESILFHYTDWVDDQRPENYREALGDV 420  
 Db 361 GABGFSKDNNSITTRKEFQEGKIFPPGVSEFGKESILFHYTDWVDDQRPENYREALGDV 420  
 QY 421 VGDYNFICPALFETKTSSEWGNNAFFYYFHRSSKLPMPBMGMVHGIELEFVGLPLER 480  
 Db 421 VGDYNFICPALFETKTSSEWGNNAFFYYFHRSSKLPMPBMGMVHGIELEFVGLPLER 480  
 QY 481 RDNYTKAEIILSRISIVKMANPAKYGNPNETONNSTSWPVKSTEOKYLTLNTESTRIMT 540  
 Db 481 RDNYTKAEIILSRISIVKMANPAKYGNPNETONNSTSWPVKSTEOKYLTLNTESTRIMT 540  
 QY 541 KLRAGQCRFWTSFPPKYLEMTGNIDEAEWEKAGFHRMNNYMDMKNQFNDYTSKESCV 600  
 Db 541 KLRAGQCRFWTSFPPKYLEMTGNIDEAEWEKAGFHRMNNYMDMKNQFNDYTSKESCV 600  
 QY 601 GL 602  
 Db 601 GL 602

RESULT 15

AAV49477  
 ID AAV49477 standard; protein; 602 AA.

AC AAV49477;  
 XX



CC decontaminate ground and buildings and equipment used to store, or  
 CC contaminated by organophosphates. The method produces esterases with  
 CC improved detoxification properties over naturally occurring  
 CC organophosphorus acid anhydride (OPAA) hydrolyzing enzymes. They are also  
 CC less likely to be inactivated by the OPAA

XX Sequence 602 AA;

Query Match 99.0%; Score 3228; DB 3; Length 602;  
 Best Local Similarity 99.3%; Pred. No. 4.4e-286;  
 Matches 598; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDSKVTITICIRFLFWFLILCMILIGKSHTEDDIIATKNGKRGVGNLTVFGSTVAFAGIP 60  
 DB 1 MHSKVTITICIRFLFWFLILCMILIGKSHTEDDIIATKNGKRGVGNLTVFGSTVAFAGIP 60  
 QY 61 YAOPLGRRLRFRKKQSLTKMSDINWATKYANSCQNDQSPFGHSEMNPNPTDLSBDC 120  
 DB 61 YAOPLGRRLRFRKKQSLTKMSDINWATKYANSCQNDQSPFGHSEMNPNPTDLSBDC 120  
 QY 121 LYLAWMIAPKPKNAATVLIWIYGGGFGTGTSLHVDGKFLARVERVIVSMNRYVAGALG 180  
 DB 121 LYLAWMIAPKPKNAATVLIWIYGGGFGTGTSLHVDGKFLARVERVIVSMNRYVAGALG 180  
 QY 181 FLALPGNPEAPGNMGLFDQOLALQWQKNTAAFGGNPKSVTLFGESAGAASVSLHLSPG 240  
 DB 181 FLALPGNPEAPGNMGLFDQOLALQWQKNTAAFGGNPKSVTLFGESAGAASVSLHLSPG 240  
 QY 241 SHSLFTRAILIQQSGFNAPMAVTSIYEARNRTLNLAKLTGCSRENTEIILKLRNKDPOEI 300  
 DB 241 SHSLFTRAILIQQSGFNAPMAVTSIYEARNRTLNLAKLTGCSRENTEIILKLRNKDPOEI 300  
 QY 301 LLINEAFVVPYGTPLSVNPGFVVDGFLTMDPDLLELGQFKKQIILGVNKGDEGTFVLVY 360  
 DB 301 LLINEAFVVPYGTPLSVNPGFVVDGFLTMDPDLLELGQFKKQIILGVNKGDEGTFVLVY 360  
 QY 361 GAGPFSKDNNSITTRKEFGGLKIFPGVSEFGKESILFHTDWDVDDQRPENYREALGDV 420  
 DB 361 GAGPFSKDNNSITTRKEFGGLKIFPGVSEFGKESILFHTDWDVDDQRPENYREALGDV 420  
 QY 421 VGDYNIICPALFETKKESEWGNNAFYFFEHRSKLPPEWVGWVGYEIEFVGLPLER 480  
 DB 421 VGDYNIICPALFETKKESEWGNNAFYFFEHRSKLPPEWVGWVGYEIEFVGLPLER 480  
 QY 481 RDNITKABEILSRISIVKMANFAKYGNDNETQNNSTSPVFKSTEOKYLTLNTESTRI 540  
 DB 481 RDNITKABEILSRISIVKMANFAKYGNDNETQNNSTSPVFKSTEOKYLTLNTESTRI 540  
 QY 541 KLRAGQCRFWTSFPKVLKEMTGNIDEAEWEMKAGFHRNNNTMDMKQFNDYTSKESCV 600  
 DB 541 KLRAGQCRFWTSFPKVLKEMTGNIDEAEWEMKAGFHRNNNTMDMKQFNDYTSKESCV 600  
 QY 601 GL 602  
 DB 601 GL 602

RESULT 17

AAV49478 ID AAY49478 standard; protein; 602 AA.

XX AC AAY49478;

XX DT 27-MAR-2000 (first entry)

XX DE Human butyryl cholinesterase (BuChE) mutant.

XX KM Organophosphate; detoxification; esterase; acetylcholinesterase; AChE;  
 KM butyrylcholinesterase; BuChE; carboxylesterase; Car; sheep dip; human;  
 XX nerve agent; organophosphorus acid anhydride; OPAA; mutant.

OS Homo sapiens.  
 OS Synthetic.

XX US6001625-A.  
 XX 14-DEC-1999.  
 XX 19-MAY-1995; 95US-00446100.  
 XX 19-MAY-1995; 95US-00446100.  
 XX (USSA ) US SEC OF ARMY.  
 XX Broomfield CA, Lockridge O, Millard CB;  
 XX WPI; 2000-096137/08.

PT Enhancing the organophosphate detoxifying capabilities of esterases for  
 PT the treatment of organophosphate poisoning.

PS Disclosure; Col 5-8; 64pp; English.

CC The invention provides a method of enhancing organophosphate detoxifying  
 CC capabilities of esterases (either human acetylcholinesterases (AChE), that  
 CC human butyrylcholinesterases (BuChE) and/or carboxylesterases (CarE), that  
 CC comprises substituting a histidine residue for 1 or more amino acid(s)  
 CC within 6 Angstrom of an active site serine. The method may be used for  
 CC enhancing organophosphate detoxifying capabilities of esterases (either  
 CC human AChE, human BuChE and/or human CarE). The modified esterases may  
 CC then be used to treat agricultural workers poisoned with organophosphates  
 CC through contact with chemical such as sheep dips. They may also be used  
 CC to treat military personnel contaminated by chemical weaponry such as  
 CC nerve agents. Additionally, the esterases may also be used to  
 CC decontaminate ground and buildings and equipment used to store, or  
 CC contaminated by organophosphates. The method produces esterases with  
 CC improved detoxification properties over naturally occurring  
 CC organophosphorus acid anhydride (OPAA) hydrolyzing enzymes. They are also  
 CC less likely to be inactivated by the OPAA

XX Sequence 602 AA;

Query Match 99.0%; Score 3228; DB 3; Length 602;  
 Best Local Similarity 99.3%; Pred. No. 4.4e-286;  
 Matches 598; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MDSKVTITICIRFLFWFLILCMILIGKSHTEDDIIATKNGKRGVGNLTVFGSTVAFAGIP 60  
 DB 1 MHSKVTITICIRFLFWFLILCMILIGKSHTEDDIIATKNGKRGVGNLTVFGSTVAFAGIP 60  
 QY 61 YAOPLGRRLRFRKKQSLTKMSDINWATKYANSCQNDQSPFGHSEMNPNPTDLSBDC 120  
 DB 61 YAOPLGRRLRFRKKQSLTKMSDINWATKYANSCQNDQSPFGHSEMNPNPTDLSBDC 120  
 QY 121 LYLAWMIAPKPKNAATVLIWIYGGGFGTGTSLHVDGKFLARVERVIVSMNRYVAGALG 180  
 DB 121 LYLAWMIAPKPKNAATVLIWIYGGGFGTGTSLHVDGKFLARVERVIVSMNRYVAGALG 180  
 QY 181 FLALPGNPEAPGNMGLFDQOLALQWQKNTAAFGGNPKSVTLFGESAGAASVSLHLSPG 240  
 DB 181 FLALPGNPEAPGNMGLFDQOLALQWQKNTAAFGGNPKSVTLFGESAGAASVSLHLSPG 240  
 QY 241 SHSLFTRAILIQQSGFNAPMAVTSIYEARNRTLNLAKLTGCSRENTEIILKLRNKDPOEI 300  
 DB 241 SHSLFTRAILIQQSGFNAPMAVTSIYEARNRTLNLAKLTGCSRENTEIILKLRNKDPOEI 300  
 QY 301 LLINEAFVVPYGTPLSVNPGFVVDGFLTMDPDLLELGQFKKQIILGVNKGDEGTFVLVY 360  
 DB 301 LLINEAFVVPYGTPLSVNPGFVVDGFLTMDPDLLELGQFKKQIILGVNKGDEGTFVLVY 360  
 QY 361 GAGPFSKDNNSITTRKEFGGLKIFPGVSEFGKESILFHTDWDVDDQRPENYREALGDV 420  
 DB 361 GAGPFSKDNNSITTRKEFGGLKIFPGVSEFGKESILFHTDWDVDDQRPENYREALGDV 420  
 QY 421 VGDYNIICPALFETKKESEWGNNAFYFFEHRSKLPPEWVGWVGYEIEFVGLPLER 480  
 DB 421 VGDYNIICPALFETKKESEWGNNAFYFFEHRSKLPPEWVGWVGYEIEFVGLPLER 480

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Db 421 VGDYNFICPALBETKPFSEWGNNAFFYFEHRSKLPMPMEGVMGSEIEFVGLPLER 480
QY 481 RDNVTKAEELLSRIVKRWANPAKYGNPNTONNSTWPFKSTEOXYTLTNTSTRIMT 540
Db 481 RDNVTKAEELLSRIVKRWANPAKYGNPNTONNSTWPFKSTEOXYTLTNTSTRIMT 540
QY 541 KLRAGQCRFWTSFPFKYLEMTGNIDEAEWEMKAGFHRMNNYMDMKQFNDYTSKESCV 600
Db 541 KLRAGQCRFWTSFPFKYLEMTGNIDEAEWEMKAGFHRMNNYMDMKQFNDYTSKESCV 600
QY 601 GL 602
Db 601 GL 602

RESULT 18
AAV49486
ID AAV49486 standard; protein; 602 AA.
AC AAV49486;
XX
XX 27-MAR-2000 (first entry)
XX
XX Human butyryl cholinesterase (BuChE) mutant.
XX
XX Organophosphate; detoxification; esterase; acetylcholinesterase; AChE;
XX butyrylcholinesterase; BuChE; carboxylesterase; CAE; sheep dip; human;
XX nerve agent; organophosphorus acid anhydride; OPAA; mutant.
XX
XX Homo sapiens.
XX OS Synthetic.
XX
XX US6001625-A.
XX
XX 14-DEC-1999.
XX
XX PF 19-MAY-1995; 95US-00446100.
XX
XX PR 19-MAY-1995; 95US-00446100.
XX
XX PA (USSA ) US SEC OF ARMY.
XX
XX Broomfield CA, Lockridge O, Millard CB;
XX
XX WPI; 2000-096137/08.
XX
XX
XX Enhancing the organophosphate detoxifying capabilities of esterases for
XX the treatment of organophosphate poisoning.
XX
XX PS Disclosure; Col 11-12; 64pp; English.
XX
XX The invention provides a method of enhancing organophosphate detoxifying
XX capabilities of esterases (either human acetylcholinesterases (AChE),
XX human butyrylcholinesterases (BuChE) and/or carboxylesterases (CAE)), that
XX comprises substituting a histidine residue for 1 or more amino acid(s)
XX within 6 Angstrom of an active site serine. The method may be used for
XX enhancing organophosphate detoxifying capabilities of esterases (either
XX human AChE, human BuChE and/or human CAE). The modified esterases may
XX then be used to treat agricultural workers poisoned with organophosphates
XX through contact with chemical such as sheep dips. They may also be used
XX to treat military personnel contaminated by chemical weapons such as
XX nerve agents. Additionally, the esterases may also be used to
XX decontaminate ground and buildings and equipment used to store, or
XX contaminated by organophosphates. The method produces esterases with
XX improved detoxification properties over naturally occurring
XX organophosphorus acid anhydride (OPAA) hydrolyzing enzymes. They are also
XX less likely to be inactivated by the OPAA
XX
XX Sequence 602 AA;
XX
XX Query Match 99.0%; Score 3227; DB 3; Length 602;
XX Best Local Similarity 99.3%; Pred. No. 5.4e-286;
XX Matches 598; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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QY 1 MDSKVTIICIRLFEMFLICMLIGKSHTEDDIIITKNGKVRGMNLTVEGTVTAFLGIP 60
Db 1 MDSKVTIICIRLFEMFLICMLIGKSHTEDDIIITKNGKVRGMNLTVEGTVTAFLGIP 60
QY 61 YAGPPLGRLEFRKKPQSLTMSDIWNATKYANSCCONIDSPFGFHSSEMANPNTDISEDC 120
Db 61 YAGPPLGRLEFRKKPQSLTMSDIWNATKYANSCCONIDSPFGFHSSEMANPNTDISEDC 120
QY 121 LYANWTIPAPKPKNAVLTWYGGGFGTSSLAHYDGEFLARVERVTVVSNMYRGAIG 180
Db 121 LYANWTIPAPKPKNAVLTWYGGGFGTSSLAHYDGEFLARVERVTVVSNMYRGAIG 180
QY 181 FLALPGRPAPGNMGLFDQOLALQWQKNIAAFGNGPKSVTLFGESAGAASVSLHLSPG 240
Db 181 FLALPGRPAPGNMGLFDQOLALQWQKNIAAFGNGPKSVTLFGESAGAASVSLHLSPG 240
QY 241 SHSLFTRAILQSGSFNAWPAVTSLYEARNRTNLAKLTCCSBNETELIKCLRNDPOBI 300
Db 241 SHSLFTRAILQSGSFNAWPAVTSLYEARNRTNLAKLTCCSBNETELIKCLRNDPOBI 300
QY 301 LLINEAFVVPYGPPLSVNPGPTVDGDLTMDPDLLELGOFKTQILVGNKDEGTFLVY 360
Db 301 LLINEAFVVPYGPPLSVNPGPTVDGDLTMDPDLLELGOFKTQILVGNKDEGTFLVY 360
QY 361 GAFGSKDNNSITTRKEFQEGKIFPPGVSEFKESILFHYTDVDDQRPENYREALGVY 420
Db 361 GAFGSKDNNSITTRKEFQEGKIFPPGVSEFKESILFHYTDVDDQRPENYREALGVY 420
QY 421 VGDYNFICPALBETKPFSEWGNNAFFYFEHRSKLPMPMEGVMGSEIEFVGLPLER 480
Db 421 VGDYNFICPALBETKPFSEWGNNAFFYFEHRSKLPMPMEGVMGSEIEFVGLPLER 480
QY 481 RDNVTKAEELLSRIVKRWANPAKYGNPNTONNSTWPFKSTEOXYTLTNTSTRIMT 540
Db 481 RDNVTKAEELLSRIVKRWANPAKYGNPNTONNSTWPFKSTEOXYTLTNTSTRIMT 540
QY 541 KLRAGQCRFWTSFPFKYLEMTGNIDEAEWEMKAGFHRMNNYMDMKQFNDYTSKESCV 600
Db 541 KLRAGQCRFWTSFPFKYLEMTGNIDEAEWEMKAGFHRMNNYMDMKQFNDYTSKESCV 600
QY 601 GL 602
Db 601 GL 602

RESULT 19
AAV49485
ID AAV49485 standard; protein; 602 AA.
AC AAV49485;
XX
XX 27-MAR-2000 (first entry)
XX
XX Human butyryl cholinesterase (BuChE) mutant.
XX
XX Organophosphate; detoxification; esterase; acetylcholinesterase; AChE;
XX butyrylcholinesterase; BuChE; carboxylesterase; CAE; sheep dip; human;
XX nerve agent; organophosphorus acid anhydride; OPAA; mutant.
XX
XX Homo sapiens.
XX OS Synthetic.
XX
XX US6001625-A.
XX
XX PF 14-DEC-1999.
XX
XX PF 19-MAY-1995; 95US-00446100.
XX
XX PR 19-MAY-1995; 95US-00446100.
XX
XX PA (USSA ) US SEC OF ARMY.
XX

```



PI Broomfield CA, Lockridge O, Millard CB;  
 XX WPI: 2000-096137/08.  
 XX  
 PT Enhancing the organophosphate detoxifying capabilities of esterases for  
 the treatment of organophosphate poisoning.  
 XX  
 PS Disclosure; Col 9-12; 64pp; English.  
 XX  
 CC The invention provides a method of enhancing organophosphate detoxifying  
 capabilities of esterases (either human acetylcholinesterases (AChE), that  
 CC human butyrylcholinesterases (BuChE) and/or carboxylesterases (CaE)), that  
 CC comprises substituting a histidine residue for 1 or more amino acid(s)  
 CC within 6 Angstrom of an active site serine. The method may be used for  
 CC enhancing organophosphate detoxifying capabilities of esterases (either  
 CC human AChE, human BuChE and/or human CaE). The modified esterases may  
 CC then be used to treat agricultural workers poisoned with organophosphates  
 CC through contact with chemical such as sheep dips. They may also be used  
 CC to treat military personnel contaminated by chemical weaponry such as  
 CC nerve agents. Additionally, the esterases may also be used to  
 CC decontaminate ground and buildings and equipment used to store, or  
 CC contaminated by organophosphates. The method produces esterases with  
 CC improved detoxification properties over naturally occurring  
 CC organophosphorus acid anhydride (OPAA) hydrolyzing enzymes. They are also  
 CC less likely to be inactivated by the OPAA  
 XX  
 SQ Sequence 602 AA;  
 Query Match 99.0%; Score 3227; DB 3; Length 602;  
 Best Local Similarity 99.3%; Pred. No. 5.4e-286;  
 Matches 598; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 MDSKVTITICIRFLFWFLLCMLIGKSHTEDDIIATKNGVGRGMNLTVFGGTYAFGIP 60  
 DB 1 MHSKVTITICIRFLFWFLLCMLIGKSHTEDDIIATKNGVGRGMNLTVFGGTYAFGIP 60  
 QY 61 YAOPPLGRLEFRKPKQSLTKMSDIWMTKYANSCCONIDQSPFGHSEMMNPNTDLSDC 120  
 DB 61 YAOPPLGRLEFRKPKQSLTKMSDIWMTKYANSCCONIDQSPFGHSEMMNPNTDLSDC 120  
 QY 121 LYANWVPAPKPKNAATVLIWYGGGFGTGTSSLAHYDGEKFLARVERIVVSMNRYVAGALG 180  
 DB 121 LYANWVPAPKPKNAATVLIWYGGGFGTGTSSLAHYDGEKFLARVERIVVSMNRYVAGALG 180  
 QY 181 PLALPGNEAPGNNGGLFDQOLALQWQKNIAPFGNPKSVTLFPSSAGASVSLHLSPG 240  
 DB 181 PLALPGNEAPGNNGGLFDQOLALQWQKNIAPFGNPKSVTLFPSSAGASVSLHLSPG 240  
 QY 241 SHSLFTTALIQSGSPNAPWATVSLYEARNRTLANLAKLTGCSRENETEIIKCLRNKDPQEI 300  
 DB 241 SHSLFTTALIQSGSPNAPWATVSLYEARNRTLANLAKLTGCSRENETEIIKCLRNKDPQEI 300  
 QY 301 LLAFAFVVPYGTPLSVNFGPTVDGFLTMDPDIILELGQFKTKOILVGNKDEGTWPLVY 360  
 DB 301 LLAFAFVVPYGTPLSVNFGPTVDGFLTMDPDIILELGQFKTKOILVGNKDEGTWPLVY 360  
 QY 361 GABGFSKDNNSITIRKEFOGLKTFPGVSEFGKESILFHFTDWDODRPNNYREALGDV 420  
 DB 361 GABGFSKDNNSITIRKEFOGLKTFPGVSEFGKESILFHFTDWDODRPNNYREALGDV 420  
 QY 421 VGDVNFICPALFETPKTSEMGNNAFYYFHEHRSKLPWEMWGVHGEIEFVGLPLER 480  
 DB 421 VGDVNFICPALFETPKTSEMGNNAFYYFHEHRSKLPWEMWGVHGEIEFVGLPLER 480  
 QY 481 RDNVTKABELISRSIVKMANPAKYGNPNTONNSTSWPVKSTOEKTLTNTSTSTIMT 540  
 DB 481 RDNVTKABELISRSIVKMANPAKYGNPNTONNSTSWPVKSTOEKTLTNTSTSTIMT 540  
 QY 541 KLRAGQCRFWTSPFKVLEMTGNIDEABEWKAGFHRNNNTMMKQNFNDYTSKKSCV 600  
 DB 541 KLRAGQCRFWTSPFKVLEMTGNIDEABEWKAGFHRNNNTMMKQNFNDYTSKKSCV 600  
 QY 601 GL 602

DB 601 GL 602  
 ||  
 RESULT 20  
 ID AAY49488 standard; protein; 602 AA.  
 AC AAY49488;  
 XX  
 XX 27-MAR-2000 (first entry)  
 DT  
 XX Human butyryl cholinesterase (BuChE) mutant.  
 DE  
 XX Organophosphate; detoxification; esterase; acetylcholinesterase; AChE;  
 KW butyrylcholinesterase; BuChE; carboxylesterase; CaE; sheep dip; human;  
 KW nerve agent; organophosphorus acid anhydride; OPAA; mutant.  
 XX  
 XX Homo sapiens.  
 OS Synthetic.  
 PN US6001625-A.  
 XX  
 PD 14-DEC-1999.  
 XX  
 PF 19-MAY-1995; 95US-00446100.  
 XX  
 PR 19-MAY-1995; 95US-00446100.  
 XX  
 PA (USSA ) US SEC OF ARMY.  
 PI Broomfield CA, Lockridge O, Millard CB;  
 XX WPI: 2000-096137/08.  
 XX  
 PT Enhancing the organophosphate detoxifying capabilities of esterases for  
 the treatment of organophosphate poisoning.  
 XX  
 PS Disclosure; Col 11-12; 64pp; English.  
 XX  
 CC The invention provides a method of enhancing organophosphate detoxifying  
 capabilities of esterases (either human acetylcholinesterases (AChE), that  
 CC human butyrylcholinesterases (BuChE) and/or carboxylesterases (CaE)), that  
 CC comprises substituting a histidine residue for 1 or more amino acid(s)  
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 CC human AChE, human BuChE and/or human CaE). The modified esterases may  
 CC then be used to treat agricultural workers poisoned with organophosphates  
 CC through contact with chemical such as sheep dips. They may also be used  
 CC to treat military personnel contaminated by chemical weaponry such as  
 CC nerve agents. Additionally, the esterases may also be used to  
 CC decontaminate ground and buildings and equipment used to store, or  
 CC contaminated by organophosphates. The method produces esterases with  
 CC improved detoxification properties over naturally occurring  
 CC organophosphorus acid anhydride (OPAA) hydrolyzing enzymes. They are also  
 CC less likely to be inactivated by the OPAA  
 XX  
 SQ Sequence 602 AA;  
 Query Match 99.0%; Score 3227; DB 3; Length 602;  
 Best Local Similarity 99.3%; Pred. No. 5.4e-286;  
 Matches 598; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 MDSKVTITICIRFLFWFLLCMLIGKSHTEDDIIATKNGVGRGMNLTVFGGTYAFGIP 60  
 DB 1 MHSKVTITICIRFLFWFLLCMLIGKSHTEDDIIATKNGVGRGMNLTVFGGTYAFGIP 60  
 QY 61 YAOPPLGRLEFRKPKQSLTKMSDIWMTKYANSCCONIDQSPFGHSEMMNPNTDLSDC 120  
 DB 61 YAOPPLGRLEFRKPKQSLTKMSDIWMTKYANSCCONIDQSPFGHSEMMNPNTDLSDC 120  
 QY 121 LYANWVPAPKPKNAATVLIWYGGGFGTGTSSLAHYDGEKFLARVERIVVSMNRYVAGALG 180

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Db      121 LYANWIPAPKPKNAATVLWITGCGFQGTGSSLAHYTDGKFLARVERVIVSMNRYVGLG 180
Qy      181 FLALPGENPAPGNMGLFDQQLALQWVQKNIAPGNGPKSVTLFGESAGAASVSLHLSFG 240
Db      181 FLALPGENPAPGNMGLFDQQLALQWVQKNIAPGNGPKSVTLFGESAGAASVSLHLSFG 240
Qy      241 SLSLFTTRAILQSGSFNAPMAVATSLYEARNRTNLAKLTGCSRENETEIIKCLRNKDPDEI 300
Db      241 SLSLFTTRAILQSGSFNAPMAVATSLYEARNRTNLAKLTGCSRENETEIIKCLRNKDPDEI 300
Qy      301 LINEAFVVPYGTPLSVNFGPTVDGDFLTMDPDLLELGQFKTQIIVGVNKGEGTWFLVY 360
Db      301 LINEAFVVPYGTPLSVNFGPTVDGDFLTMDPDLLELGQFKTQIIVGVNKGEGTWFLVY 360
Qy      361 GAPGFSKDNNSITTRKEFOEGKIFPPGVSEFGKESILFHYTDWDDQRENTREALGV 420
Db      361 GAPGFSKDNNSITTRKEFOEGKIFPPGVSEFGKESILFHYTDWDDQRENTREALGV 420
Qy      421 VGDYNFICPALFETFKKSEMGNNAFYYFPEHRSKLPWPMGVGMHGYEIEFVFGPLER 480
Db      421 VGDYNFICPALFETFKKSEMGNNAFYYFPEHRSKLPWPMGVGMHGYEIEFVFGPLER 480
Qy      481 RDNTYKAEILSRISIVKMANFAKYGNPNETONNSTMPVFKSTQKYLTLNTESTRIIMT 540
Db      481 RDNTYKAEILSRISIVKMANFAKYGNPNETONNSTMPVFKSTQKYLTLNTESTRIIMT 540
Qy      541 KLRAGQCRFWTSFPPKYLEMTGNIDEAEWEKAGFRHNNYMMDMKNOFNDYTSKESCV 600
Db      541 KLRAGQCRFWTSFPPKYLEMTGNIDEAEWEKAGFRHNNYMMDMKNOFNDYTSKESCV 600
Qy      601 GL 602
Db      601 GL 602

RESULT 21
AA49487
ID      AA49487 standard; protein; 602 AA.
AC      AA49487;
DT      27-MAR-2000 (first entry)
XX
DE      Human butyryl cholinesterase (BuChE) mutant.
XX
KW      Organophosphate; detoxification; esterase; acetylcholinesterase; AChE;
KW      butyrylcholinesterase; BuChE; carboxylesterase; CaE; sheep dlp; human;
KW      nerve agent; organophosphorus acid anhydride; OPAA; mutant.
XX
OS      Homo sapiens.
XX
XX      Synthetic.
XX
XX      US6001625-A.
XX
XX      14-DEC-1999.
XX
XX      19-MAY-1995; 95US-00446100.
XX
XX      19-MAY-1995; 95US-00446100.
XX
XX      (USSA ) US SEC OF ARMY.
XX
XX      Broomfield CA, Lockridge O, Millard CB;
XX
XX      WPI; 2000-096137/08.
XX
XX      Enhancing the organophosphate detoxifying capabilities of esterases for
XX      the treatment of organophosphate poisoning.
XX
XX      Disclosure; Col 11-12; 64pp; English.
XX
XX      The invention provides a method of enhancing organophosphate detoxifying
XX      capabilities of esterases (either human acetylcholinesterases (AChE),
XX

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CC      human butyrylcholinesterases (BuChE) and/or carboxylesterases (CaE), that
CC      comprises substituting a histidine residue for 1 or more amino acid(s)
CC      within 6 Angstrom of an active site serine. The method may be used for
CC      enhancing organophosphate detoxifying capabilities of esterases (either
CC      human AChE, human BuChE and/or human CaE). The modified esterases may
CC      then be used to treat agricultural workers poisoned with organophosphates
CC      through contact with chemical such as sheep dips. They may also be used
CC      to treat military personnel contaminated by chemical weapons such as
CC      nerve agents. Additionally, the esterases may also be used to
CC      decontaminate ground and buildings and equipment used to store, or
CC      contaminated by organophosphates. The method produces esterases with
CC      improved detoxification properties over naturally occurring
CC      organophosphorus acid anhydride (OPAA) hydrolyzing enzymes. They are also
CC      less likely to be inactivated by the OPAA.
XX
XX      Sequence 602 AA;
SQ
Query Match      99.0%; Score 3226; DB 3; Length 602;
Best Local Similarity 99.3%; Pred. No. 6.7e-286;
Matches 598; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy      1 MSKVTIICIRPLFWFLICMLIGKSHTEDDIIATKNGKVRGNLTVFGGTVAFLGIP 60
Db      1 MSKVTIICIRPLFWFLICMLIGKSHTEDDIIATKNGKVRGNLTVFGGTVAFLGIP 60
Qy      61 YAOPLGLRLFRKQPSLTIRKMSDINWATYANSCCONIDQSPFGHSGEMNPNPDLSDC 120
Db      61 YAOPLGLRLFRKQPSLTIRKMSDINWATYANSCCONIDQSPFGHSGEMNPNPDLSDC 120
Qy      121 LYANWIPAPKPKNAATVLWITGCGFQGTGSSLAHYTDGKFLARVERVIVSMNRYVGLG 180
Db      121 LYANWIPAPKPKNAATVLWITGCGFQGTGSSLAHYTDGKFLARVERVIVSMNRYVGLG 180
Qy      181 FLALPGENPAPGNMGLFDQQLALQWVQKNIAPGNGPKSVTLFGESAGAASVSLHLSFG 240
Db      181 FLALPGENPAPGNMGLFDQQLALQWVQKNIAPGNGPKSVTLFGESAGAASVSLHLSFG 240
Qy      241 SLSLFTTRAILQSGSFNAPMAVATSLYEARNRTNLAKLTGCSRENETEIIKCLRNKDPDEI 300
Db      241 SLSLFTTRAILQSGSFNAPMAVATSLYEARNRTNLAKLTGCSRENETEIIKCLRNKDPDEI 300
Qy      301 LINEAFVVPYGTPLSVNFGPTVDGDFLTMDPDLLELGQFKTQIIVGVNKGEGTWFLVY 360
Db      301 LINEAFVVPYGTPLSVNFGPTVDGDFLTMDPDLLELGQFKTQIIVGVNKGEGTWFLVY 360
Qy      361 GAPGFSKDNNSITTRKEFOEGKIFPPGVSEFGKESILFHYTDWDDQRENTREALGV 420
Db      361 GAPGFSKDNNSITTRKEFOEGKIFPPGVSEFGKESILFHYTDWDDQRENTREALGV 420
Qy      421 VGDYNFICPALFETFKKSEMGNNAFYYFPEHRSKLPWPMGVGMHGYEIEFVFGPLER 480
Db      421 VGDYNFICPALFETFKKSEMGNNAFYYFPEHRSKLPWPMGVGMHGYEIEFVFGPLER 480
Qy      481 RDNTYKAEILSRISIVKMANFAKYGNPNETONNSTMPVFKSTQKYLTLNTESTRIIMT 540
Db      481 RDNTYKAEILSRISIVKMANFAKYGNPNETONNSTMPVFKSTQKYLTLNTESTRIIMT 540
Qy      541 KLRAGQCRFWTSFPPKYLEMTGNIDEAEWEKAGFRHNNYMMDMKNOFNDYTSKESCV 600
Db      541 KLRAGQCRFWTSFPPKYLEMTGNIDEAEWEKAGFRHNNYMMDMKNOFNDYTSKESCV 600
Qy      601 GL 602
Db      601 GL 602

RESULT 22
AA49482
ID      AA49482 standard; protein; 602 AA.
AC      AA49482;
DT      27-MAR-2000 (first entry)

```

XX Human butyryl cholinesterase (BuChE) mutant.  
 XX Organophosphate; detoxification; esterase; acetylcholinesterase; AChE;  
 KW butyrylcholinesterase; BuChE; carboxylesterase; CaE; sheep dip; human;  
 KW nerve agent; organophosphorus acid anhydride; OPA; mutant.  
 XX Homo sapiens.  
 OS Synthetic.  
 PN US6001625-A.  
 PD 14-DEC-1999.  
 PF 19-MAY-1995; 95US-00446100.  
 PR 19-MAY-1995; 95US-00446100.  
 PA (USSA ) US SEC OF ARMY.  
 PI Broomfield CA, Lockridge O, Millard CB;  
 DR WPI; 2000-096137/08.  
 PT Enhancing the organophosphate detoxifying capabilities of esterases for  
 XX the treatment of organophosphate poisoning.  
 PS Disclosure; Col 9-10; 64pp; English.  
 XX The invention provides a method of enhancing organophosphate detoxifying  
 CC capabilities of esterases (either human acetylcholinesterases (AChE),  
 CC human butyrylcholinesterases (BuChE) and/or carboxylesterases (CaE)), that  
 CC comprises substituting a histidine residue for 1 or more amino acid(s)  
 CC within 6 Angstrom of an active site serine. The method may be used for  
 CC enhancing organophosphate detoxifying capabilities of esterases (either  
 CC human AChE, human BuChE and/or human CaE). The modified esterases may  
 CC then be used to treat agricultural workers poisoned with organophosphates  
 CC through contact with chemical such as sheep dips. They may also be used  
 CC to treat military personnel contaminated by chemical weaponry such as  
 CC nerve agents. Additionally, the esterases may also be used to  
 CC decontaminate ground and buildings and equipment used to store, or  
 CC contaminated by organophosphates. The method produces esterases with  
 CC improved detoxification properties over naturally occurring  
 CC organophosphorus acid anhydride (OPA) hydrolyzing enzymes. They are also  
 CC less likely to be inactivated by the OPA.  
 XX  
 SQ Sequence 602 AA;  
 Query Match 98.9%; Score 3225; DB 3; Length 602;  
 Best Local Similarity 99.3%; Pred. No. 8.2e-266;  
 Matches 598; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 MDSKVTIIICIRFLFWPLLCLMICKSHTEDDIIATKNGKVRGNLTVFGTVAFLGIP 60  
 DB 1 MHSKVTIIICIRFLFWPLLCLMICKSHTEDDIIATKNGKVRGNLTVFGTVAFLGIP 60  
 QY 61 YAOPLGLRLRKKQSLTKMSDINWATKYANSCONIDOSPFGHSGEMNPNPDLSEDC 120  
 DB 61 YAOPLGLRLRKKQSLTKMSDINWATKYANSCONIDOSPFGHSGEMNPNPDLSEDC 120  
 QY 121 LYLVNWIIPAPKPKNAATLIIWYGGFOTGTSLLHVVQDKFLARVERVIVSMNRYVAGALG 180  
 DB 121 LYLVNWIIPAPKPKNAATLIIWYGGFOTGTSLLHVVQDKFLARVERVIVSMNRYVAGALG 180  
 QY 181 FLALPGNPEAPNGNGLFDQOLALQWVQKNIAPFGSNPKSVTLFGESAGAAVSILHLLSPG 240  
 DB 181 FLALPGNPEAPNGNGLFDQOLALQWVQKNIAPFGSNPKSVTLFGESAGAAVSILHLLSPG 240  
 QY 241 SHSIFTRAILLOSGFNAPWATSIYEARNRNLNAKLTCGRREMETRIKLRKDDPEI 300  
 DB 241 SHSIFTRAILLOSGFNAPWATSIYEARNRNLNAKLTCGRREMETRIKLRKDDPEI 300  
 QY 301 LLINEAFVVPYGTPLSVNFGPTVDGDFLTDMPDILLELQGFKKQILVGVNKDEGTWFLVY 360

DB 301 LLINEAFVVPYGTPLSVNFGPTVDGDFLTDMPDILLELQGFKKQILVGVNKDEGTWFLVY 360  
 QY 361 GARGFSKDNNSIITRKRFQGLKIPFGVSEFGKESILFYTYMVDQRPENYREALGDV 420  
 DB 361 GARGFSKDNNSIITRKRFQGLKIPFGVSEFGKESILFYTYMVDQRPENYREALGDV 420  
 QY 421 VGDYNIICPALIEFTKKSEWGNNAFFYYFEHRSSKLPWPEMGMVHGYLEIFVGLPLER 480  
 DB 421 VGDYNIICPALIEFTKKSEWGNNAFFYYFEHRSSKLPWPEMGMVHGYLEIFVGLPLER 480  
 QY 481 RDNVTKAEIILSRSIYKRWANPAKYGNDPNTONNSTSWPFKSTEQKYLTLNTESTIMT 540  
 DB 481 RDNVTKAEIILSRSIYKRWANPAKYGNDPNTONNSTSWPFKSTEQKYLTLNTESTIMT 540  
 QY 541 KLRAGQCRFTWTSFPFKVLEMTGNIDEAEMEMKAGFHRMNNYMMDMKQFNDYSKKESCV 600  
 DB 541 KLRAGQCRFTWTSFPFKVLEMTGNIDEAEMEMKAGFHRMNNYMMDMKQFNDYSKKESCV 600  
 QY 601 GL 602  
 DB 601 GL 602  
 RESULT 23  
 ID AAY49481  
 AA AAY49481 standard; protein; 602 AA.  
 AC AAY49481;  
 XX 27-MAR-2000 (first entry)  
 XX Human butyryl cholinesterase (BuChE) mutant.  
 DE Organophosphate; detoxification; esterase; acetylcholinesterase; AChE;  
 KW butyrylcholinesterase; BuChE; carboxylesterase; CaE; sheep dip; human;  
 KW nerve agent; organophosphorus acid anhydride; OPA; mutant.  
 XX Homo sapiens.  
 OS Synthetic.  
 PN US6001625-A.  
 PD 14-DEC-1999.  
 PF 19-MAY-1995; 95US-00446100.  
 PR 19-MAY-1995; 95US-00446100.  
 PA (USSA ) US SEC OF ARMY.  
 PI Broomfield CA, Lockridge O, Millard CB;  
 DR WPI; 2000-096137/08.  
 PT Enhancing the organophosphate detoxifying capabilities of esterases for  
 XX the treatment of organophosphate poisoning.  
 PS Disclosure; Col 7-8; 64pp; English.  
 XX The invention provides a method of enhancing organophosphate detoxifying  
 CC capabilities of esterases (either human acetylcholinesterases (AChE),  
 CC human butyrylcholinesterases (BuChE) and/or carboxylesterases (CaE)), that  
 CC comprises substituting a histidine residue for 1 or more amino acid(s)  
 CC within 6 Angstrom of an active site serine. The method may be used for  
 CC enhancing organophosphate detoxifying capabilities of esterases (either  
 CC human AChE, human BuChE and/or human CaE). The modified esterases may  
 CC then be used to treat agricultural workers poisoned with organophosphates  
 CC through contact with chemical such as sheep dips. They may also be used  
 CC to treat military personnel contaminated by chemical weaponry such as  
 CC nerve agents. Additionally, the esterases may also be used to  
 CC decontaminate ground and buildings and equipment used to store, or  
 CC contaminated by organophosphates. The method produces esterases with

CC Improved detoxification properties over naturally occurring  
 CC organophosphorus acid anhydride (OPAA) hydrolyzing enzymes. They are also  
 CC less likely to be inactivated by the OPAA

XX Sequence 602 AA;

Query Match 98.9%; Score 3224; DB 3; Length 602;

Best Local Similarity 99.3%; Pred. No. 1e-285; Mismatches 4; Indels 0; Gaps 0;

Matches 598; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDSKVTITICRFLFWFLLLCMLIGKSTHEDDIIATKNGKVRGMNLTVEGTTATFLGIP 60  
 DB 1 MHSKVTITICRFLFWFLLLCMLIGKSTHEDDIIATKNGKVRGMNLTVEGTTATFLGIP 60  
 QY 61 YAOPLGLRLFRKPOSILTKMSDIWNAATKYANSCCONIDSPFGHSEMMNPTDLSDEC 120  
 DB 61 YAOPLGLRLFRKPOSILTKMSDIWNAATKYANSCCONIDSPFGHSEMMNPTDLSDEC 120  
 QY 121 LYNWVWPAPKPKNAATVLIWYGGGFQGTSSLHVYDGKFLARVERVIVSMNYRVGALG 180  
 DB 121 LYNWVWPAPKPKNAATVLIWYGGGFQGTSSLHVYDGKFLARVERVIVSMNYRVGALG 180  
 QY 181 FLALPGNPEAPGNMGLFDQOLALQWOKNTAARGNPKSVTLFGESAGASVSLHLISPG 240  
 DB 181 FLALPGNPEAPGNMGLFDQOLALQWOKNTAARGNPKSVTLFGESAGASVSLHLISPG 240  
 QY 241 SHSLFTRAILIQQSGSFNAPMAVTSLYEARNRTLANAKLTGCSRENETEIIKCLRNKPOEI 300  
 DB 241 SHSLFTRAILIQQSGSFNAPMAVTSLYEARNRTLANAKLTGCSRENETEIIKCLRNKPOEI 300  
 QY 301 LNEAFVVPYGTPLSVNFGPTVDGDLTMDPDIILELQGFKTQIILVGNKDEGTWFLVY 360  
 DB 301 LNEAFVVPYGTPLSVNFGPTVDGDLTMDPDIILELQGFKTQIILVGNKDEGTWFLVY 360  
 QY 361 GARGFSKDNNSITTRKEFOGLKIFPGVSEFKESILFHTYDWDQRENTREALGDV 420  
 DB 361 GARGFSKDNNSITTRKEFOGLKIFPGVSEFKESILFHTYDWDQRENTREALGDV 420  
 QY 421 VGDYNFICPALFETKFSSEMNNAFFYYFHRSSKLPMPBMGMVMGCEIEIEFVGLPLER 480  
 DB 421 VGDYNFICPALFETKFSSEMNNAFFYYFHRSSKLPMPBMGMVMGCEIEIEFVGLPLER 480  
 QY 481 RDNYYKAEIISRSIVKMANFAKYNPNETONNSTSPVFKSTEQKYLTLNTESTRIMT 540  
 DB 481 RDNYYKAEIISRSIVKMANFAKYNPNETONNSTSPVFKSTEQKYLTLNTESTRIMT 540  
 QY 541 KLRAGQCRFWTSFPPKYLEMTGNIDEAEWEKAGFHRNNYMMQNDYTSKESCV 600  
 DB 541 KLRAGQCRFWTSFPPKYLEMTGNIDEAEWEKAGFHRNNYMMQNDYTSKESCV 600  
 QY 601 GL 602  
 DB 601 GL 602

RESULT 24

AA49480 ID AA49480 standard; protein; 602 AA.

AA49480;

27-MAR-2000 (first entry)

Human butyryl cholinesterase (BuChE) mutant.

Organophosphate; detoxification; esterase; acetylcholinesterase; AChE;

butyrylcholinesterase; BuChE; carboxylesterase; CaE; sheep dip; human;

nerve agent; organophosphorus acid anhydride; OPAA; mutant.

Homo sapiens.

Synthetic.

US6001625-A.

XX 14-DEC-1999.  
 PD 19-MAY-1995; 95US-00446100.  
 XX 19-MAY-1995; 95US-00446100.  
 XX (USSA ) US SEC OF ARMY.  
 PA Broomfield CA, Lockridge O, Millard CB;  
 PI WPI, 2000-096137/08.  
 XX Enhancing the organophosphate detoxifying capabilities of esterases for  
 PT the treatment of organophosphate poisoning.  
 PS Disclosure; Col 7-8; 64pp; English.

CC The invention provides a method of enhancing organophosphate detoxifying  
 CC capabilities of esterases (either human acetylcholinesterases (AChE), that  
 CC human butyrylcholinesterases (BuChE) and/or carboxylesterases (CaE)), that  
 CC comprises substituting a histidine residue for 1 or more amino acid(s)  
 CC within 6 Angstrom of an active site serine. The method may be used for  
 CC enhancing organophosphate detoxifying capabilities of esterases (either  
 CC human AChE, human BuChE and/or human CaE). The modified esterases may  
 CC then be used to treat agricultural workers poisoned with organophosphates  
 CC through contact with chemical such as sheep dips. They may also be used  
 CC to treat military personnel contaminated by chemical weaponry such as  
 CC nerve agents. Additionally, the esterases may also be used to  
 CC decontaminate ground and buildings and equipment used to store, or  
 CC contaminated by organophosphates. The method produces esterases with  
 CC improved detoxification properties over naturally occurring  
 CC organophosphorus acid anhydride (OPAA) hydrolyzing enzymes. They are also  
 CC less likely to be inactivated by the OPAA

Sequence 602 AA;

Query Match 98.9%; Score 3223; DB 3; Length 602;

Best Local Similarity 99.3%; Pred. No. 1.3e-285; Mismatches 4; Indels 0; Gaps 0;

Matches 598; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDSKVTITICRFLFWFLLLCMLIGKSTHEDDIIATKNGKVRGMNLTVEGTTATFLGIP 60  
 DB 1 MHSKVTITICRFLFWFLLLCMLIGKSTHEDDIIATKNGKVRGMNLTVEGTTATFLGIP 60  
 QY 61 YAOPLGLRLFRKPOSILTKMSDIWNAATKYANSCCONIDSPFGHSEMMNPTDLSDEC 120  
 DB 61 YAOPLGLRLFRKPOSILTKMSDIWNAATKYANSCCONIDSPFGHSEMMNPTDLSDEC 120  
 QY 121 LYNWVWPAPKPKNAATVLIWYGGGFQGTSSLHVYDGKFLARVERVIVSMNYRVGALG 180  
 DB 121 LYNWVWPAPKPKNAATVLIWYGGGFQGTSSLHVYDGKFLARVERVIVSMNYRVGALG 180  
 QY 181 FLALPGNPEAPGNMGLFDQOLALQWOKNTAARGNPKSVTLFGESAGASVSLHLISPG 240  
 DB 181 FLALPGNPEAPGNMGLFDQOLALQWOKNTAARGNPKSVTLFGESAGASVSLHLISPG 240  
 QY 241 SHSLFTRAILIQQSGSFNAPMAVTSLYEARNRTLANAKLTGCSRENETEIIKCLRNKPOEI 300  
 DB 241 SHSLFTRAILIQQSGSFNAPMAVTSLYEARNRTLANAKLTGCSRENETEIIKCLRNKPOEI 300  
 QY 301 LNEAFVVPYGTPLSVNFGPTVDGDLTMDPDIILELQGFKTQIILVGNKDEGTWFLVY 360  
 DB 301 LNEAFVVPYGTPLSVNFGPTVDGDLTMDPDIILELQGFKTQIILVGNKDEGTWFLVY 360  
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 DB 361 GARGFSKDNNSITTRKEFOGLKIFPGVSEFKESILFHTYDWDQRENTREALGDV 420  
 QY 421 VGDYNFICPALFETKFSSEMNNAFFYYFHRSSKLPMPBMGMVMGCEIEIEFVGLPLER 480  
 DB 421 VGDYNFICPALFETKFSSEMNNAFFYYFHRSSKLPMPBMGMVMGCEIEIEFVGLPLER 480

QY 481 RDNTKAEILSRISIVKMANPAKYGNNPNTONNSTSWPVFKSTEQKYLTLNTESTRIMT 540  
 DB 481 RDNTKAEILSRISIVKMANPAKYGNNPNTONNSTSWPVFKSTEQKYLTLNTESTRIMT 540  
 QY 541 KLRNQCRFWTSFPPKYLEMTGNIDEAEWEMKAGFHRNNYMDWKQFNDYTSKESCV 600  
 DB 541 KLRNQCRFWTSFPPKYLEMTGNIDEAEWEMKAGFHRNNYMDWKQFNDYTSKESCV 600  
 QY 601 GL 602  
 DB 601 GL 602  
 RESULT 25  
 AAY49479  
 ID AAY49479 standard; protein; 602 AA.  
 AC AAY49479;  
 XX 27-MAR-2000 (first entry)  
 DE Human butyryl cholinesterase (BuChE) mutant.  
 KM Organophosphate; detoxification; esterase; acetylcholinesterase; AChE;  
 KM butyrylcholinesterase; BuChE; carboxylesterase; Cab; sheep dip; human;  
 KM nerve agent; organophosphorus acid anhydride; OPAA; mutant.  
 OS Homo sapiens.  
 OS Synthetic.  
 XX US6001625-A.  
 PN 14-DEC-1999.  
 PD 19-MAY-1995; 95US-00446100.  
 PR 19-MAY-1995; 95US-00446100.  
 XX (USSA ) US SEC OF ARMY.  
 PA Broomfield CA, Lockridge O, Millard CB;  
 PI WPI; 2000-096137/08.  
 DR Enhancing the organophosphate detoxifying capabilities of esterases for  
 PT the treatment of organophosphate poisoning.  
 XX Disclosure; Col 7-8; 64pp; English.  
 PS The invention provides a method of enhancing organophosphate detoxifying  
 CC capabilities of esterases (either human acetylcholinesterases (AChE), that  
 CC human butyrylcholinesterases (BuChE) and/or carboxylesterases (Cab), that  
 CC comprises substituting a histidine residue for I or more amino acid(s)  
 CC within 6 Angstrom of an active site serine. The method may be used for  
 CC enhancing organophosphate detoxifying capabilities of esterases (either  
 CC human AChE, human BuChE and/or human Cab). The modified esterases may  
 CC then be used to treat agricultural workers poisoned with organophosphates  
 CC through contact with chemical such as sheep dips. They may also be used  
 CC to treat military personnel contaminated by chemical weaponry such as  
 CC nerve agents. Additionally, the esterases may also be used to  
 CC decontaminate ground and buildings and equipment used to store, or  
 CC contaminated by organophosphates. The method produces esterases with  
 CC improved detoxification properties over naturally occurring  
 CC organophosphorus acid anhydride (OPAA) hydrolyzing enzymes. They are also  
 CC less likely to be inactivated by the OPAA  
 XX Sequence 602 AA;  
 SQ  
 Query Match 98.9%; Score 323; DB 3; Length 602;  
 Best Local Similarity 99.3%; Pred. No. 1.3e-285;  
 Matches 598; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 MDSKVTIICIRFLFWFLLCMLIGKSHTEDDIIATKNGKVRGNLTVFGGTVAFLGIP 60

DB 1 MDSKVTIICIRFLFWFLLCMLIGKSHTEDDIIATKNGKVRGNLTVFGGTVAFLGIP 60  
 QY YAOPLGRLEKPKQSLTKMSDIWNATKYNSSCCONIDQSPFGHSEMMNPNTDLSBDC 120  
 DB 61 YAOPLGRLEKPKQSLTKMSDIWNATKYNSSCCONIDQSPFGHSEMMNPNTDLSBDC 120  
 QY 121 LYLNWMIAPKPKKATVLIWYGGGFGTGSLSHVYDGKFLARVERIVVSMNYRVGALG 180  
 DB 121 LYLNWMIAPKPKKATVLIWYGGGFGTGSLSHVYDGKFLARVERIVVSMNYRVGALG 180  
 QY 181 FLALPGNPEAPGNWGLFDQOLALQWOKNIAAAGGNPKSYTLFGESAGAAVSLSHLSPG 240  
 DB 181 FLALPGNPEAPGNWGLFDQOLALQWOKNIAAAGGNPKSYTLFGESAGAAVSLSHLSPG 240  
 QY 241 SHSLFTRAILIOSGSPNAPVATSLYEARNRTLNLAKLTGSRNRETEIICLRNKDPOEI 300  
 DB 241 SHSLFTRAILIOSGSPNAPVATSLYEARNRTLNLAKLTGSRNRETEIICLRNKDPOEI 300  
 QY 301 LLINEAFVVPYGTPLSVNFGPTVDGDFLTDPDILLBLGQFKTKQILVGNKDEGTWFLVY 360  
 DB 301 LLINEAFVVPYGTPLSVNFGPTVDGDFLTDPDILLBLGQFKTKQILVGNKDEGTWFLVY 360  
 QY 361 GARGFSKONNSITTRKEFGGLKIFPPGVSEFGKESILFHYTWDQRENTREALGDV 420  
 DB 361 GARGFSKONNSITTRKEFGGLKIFPPGVSEFGKESILFHYTWDQRENTREALGDV 420  
 QY 421 VGDYNFICPALFETKKSEWGNNAFFYYFEHRSKLPMPMGVMGHEYLEFVGLPLER 480  
 DB 421 VGDYNFICPALFETKKSEWGNNAFFYYFEHRSKLPMPMGVMGHEYLEFVGLPLER 480  
 QY 481 RDNTKAEILSRISIVKMANPAKYGNNPNTONNSTSWPVFKSTEQKYLTLNTESTRIMT 540  
 DB 481 RDNTKAEILSRISIVKMANPAKYGNNPNTONNSTSWPVFKSTEQKYLTLNTESTRIMT 540  
 QY 541 KLRNQCRFWTSFPPKYLEMTGNIDEAEWEMKAGFHRNNYMDWKQFNDYTSKESCV 600  
 DB 541 KLRNQCRFWTSFPPKYLEMTGNIDEAEWEMKAGFHRNNYMDWKQFNDYTSKESCV 600  
 QY 601 GL 602  
 DB 601 GL 602

Search completed: January 6, 2005, 09:37:30  
 Job time : 165 secs

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OM protein - protein search, using sw model

Run on: January 6, 2005, 09:42:34 ; Search time 197 Seconds

(without alignments)  
1676.472 Million cell updates/sec

Title: US-09-748-739a-2\_COPY\_29\_602

Perfect score: 3110  
Sequence: 1 EDDIIITATKNGKVRGNLTV.....MDMKNGPDYTSKSCVGL 574

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 100 summaries

Database : UniProt\_02:.\*  
1: \_uniprot\_sprot:.\*  
2: \_uniprot\_trembl:.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3096	99.5	602	1	CHLE_HUMAN
2	2843	91.4	581	1	CHLE_RABIT
3	2775	89.2	602	2	GNIN9
4	2774	89.2	574	1	CHLE_HORSE
5	2696	86.7	602	1	CHLE_FELCA
6	2684	86.3	602	1	CHLE_PAVTT
7	2530.	81.4	603	2	BAC34196
8	2521	81.1	603	1	CHLE_MOUSE
9	2505	80.5	597	2	O9JFC1
10	2289	73.6	603	2	O90ZK8
11	1765.5	56.8	634	1	ACES_BRARE
12	1765	56.8	633	1	ACES_ELEBL
13	1722.5	55.4	606	1	ACES_BUNFA
14	1689	54.3	614	1	ACES_HUMAN
15	1689	54.3	614	2	APP2365
16	1678.5	54.0	614	2	ACES_RAT
17	1675.5	53.9	614	1	ACES_MOUSE
18	1675.5	53.9	614	2	BAC31228
19	1675.5	53.9	614	2	BAC31641
20	1675.5	53.8	614	2	BAC32595
21	1674	53.8	349	2	O9GKJ6
22	1666.5	53.5	611	1	ACES_BOVCA
23	1663.5	53.5	613	1	ACES_PELCA
24	1649.5	53.0	584	1	ACES_RABIT
25	1649	53.0	586	1	ACES_TORNA
26	1648	53.0	586	1	ACES_TORCA
27	1557.5	50.1	717	2	ACES_TMR9
28	1455.5	46.8	767	2	ACES_CHICK
29	1435	46.1	602	2	O76959
30	1376	44.2	605	2	O76998
31	1358	43.7	526	2	O86YX9

32	1323	42.5	701	2	O75VX9
33	1323	42.5	701	2	BAD06210
34	1317	42.3	702	1	ACES_CULPI
35	1302	41.9	623	1	O7RTM0
36	1302	41.9	737	1	ACES_AMOGA
37	1302	41.9	743	2	O7PUR2
38	1294	41.6	559	2	O7PKM1
39	1273	40.9	687	2	O86C24
40	1220	39.2	666	2	O9BMJ1
41	1216	39.1	670	2	O6KAV3
42	1213	39.0	671	2	O6KAV4
43	1212	39.0	676	2	O8MW35
44	1209	38.9	675	2	O6KAV5
45	1195	38.4	610	2	O9J110
46	1177.5	37.9	677	2	O9NTH6
47	1172	37.7	656	2	O96529
48	1166	37.5	656	2	O9XYA9
49	1146	36.8	638	2	O86QW5
50	1145	36.8	620	1	ACES_CABBR
51	1143	36.8	647	2	O8MX85
52	1142	36.7	620	1	ACES_CABEL
53	1135	36.5	629	1	ACES_LEPDE
54	1129	36.3	638	2	O8MZL2
55	1127	36.2	585	2	O7RTL6
56	1088.5	35.0	550	2	O7RTL7
57	1079	34.7	587	2	O6XR74
58	1079	34.7	587	2	AAP49302
59	1079	34.7	593	2	O6XR75
60	1079	34.7	593	2	AAP49301
61	1073	34.5	530	2	O61987
62	1070.5	34.4	637	2	O9TX11
63	1065	34.2	596	2	O6XR73
64	1065	34.2	596	2	AAP49303
65	1063.5	34.2	645	2	O7ORF0
66	1063.5	34.2	645	2	O7RTL9
67	1059.5	34.1	664	1	ACES_ANOST
68	1055.5	33.9	633	2	O75VY0
69	1055.5	33.9	633	2	BAD06209
70	1045.5	33.6	692	2	O95P20
71	1045.5	33.6	692	2	O95WV7
72	1045	33.6	595	2	O45210
73	1044	33.6	649	1	ACES_DROME
74	1043.5	33.6	692	2	O8MXC6
75	1043.5	33.6	692	2	O8MXC8
76	1043.5	33.6	692	2	O8MXC9
77	1042.5	33.5	510	2	O7YZP7
78	1040.5	33.5	692	2	O8MXC4
79	1038.5	33.4	612	2	O8MW09
80	1037.5	33.4	692	2	O8MXC5
81	1036.5	33.3	692	2	O8MXC7
82	1033.5	33.2	664	2	O8RTU9
83	1029.5	33.1	708	2	P91954
84	1028.5	33.1	692	2	O7YW09
85	1027.5	33.0	673	2	O8MW24
86	1024.5	32.9	603	2	O7YZC0
87	1019.5	32.8	528	2	O62563
88	1019.5	32.8	604	1	ACES_CABRR
89	1014.5	32.6	338	1	ACES_MYXGL
90	1013	32.6	664	2	O8MW36
91	1012.5	32.6	602	2	O61372
92	1008	32.4	461	2	O7YZP8
93	959	30.8	492	2	O9GQP7
94	957	30.8	615	2	O86GL7
95	954	30.7	512	2	O8MZM0
96	948	30.5	629	2	O61371
97	946	30.4	629	2	O61378
98	944	30.4	592	2	O6QDP4
99	944	30.4	592	2	AAS49411
100	943	30.3	604	2	O9NDG9

## ALIGNMENTS

O75VX9	culx trita
BAD06210	culx trt
O86968	culx pipie
O7RTM0	anopheles g
O86963	anopheles g
O7PUR2	anopheles g
O7PKM1	anopheles g
O86C24	tetranichus
O9BMJ1	schizaphis
O6KAV3	aphis gossy
O6KAV4	aphis gossy
O8MW35	aphis gossy
O6KAV5	aphis gossy
O9J110	lo1lgo opai
O9NTH6	nephroetix
O96529	meioidogyne
O9XYA9	meioidogyne
O86QW5	helicoverpa
O8MX85	helicoverpa
O8MX85	caenorhabdi
P38433	caenorhabdi
O27677	leptinotars
O8MZL2	plutella xy
O7RTL6	clona intes
O7RTL7	clona bavig
O6XR74	rhipicephal
AAP49302	rhipiceph
O6XR75	rhipiceph
AAP49301	rhipiceph
O61987	boophilus d
O9TX11	aedes aegy
O6XR73	dermacentor
AAP49303	dermacent
O7ORF0	anopheles g
O7RTL9	anopheles g
O75VY0	culx trita
BAD06209	culx trt
O95P20	musca domes
O95WV7	musca domes
O45210	boophilus m
P07110	drosophila
O8MXC6	musca domes
O8MXC8	musca domes
O8MXC9	musca domes
O7YZP7	trialeurode
O8MXC4	musca domes
O8MW09	musca domes
O8MXC5	musca domes
O8MXC7	musca domes
O8RTU9	musca domes
P91954	lucilia cup
O7YW09	musca domes
O8MW24	bactrocera
O7YZC0	myzus persi
O62563	rhipicephal
O8MXC7	rhipicephal
O8RTU9	caenorhabdi
P91954	caenorhabdi
O7YW09	myxine glut
O8MW24	aphis gossy
O61372	caenorhabdi
O7YZP8	bemisia tab
O9GQP7	aple mellif
O86GL7	dicyocanul
O8MZM0	plutella xy
O61371	caenorhabdi
O61378	caenorhabdi
O6QDP4	dicyocanul
AAS49411	dicyocanul
O9NDG9	caenorhabdi

RESULT 1  
CHLE\_HUMAN STANDARD; PRT; 602 AA.  
ID CHLE\_HUMAN  
AC P06276;  
DT 01-JAN-1988 (Rel. 06, Created)  
DT 01-AUG-1988 (Rel. 08, Last sequence update)  
DT 01-OCT-2004 (Rel. 45, Last annotation update)  
DE Cholinesterase precursor (EC 3.1.1.8) (Acylcholine acylhydrolase)  
DE (choline esterase II) (Butyrylcholine esterase)  
DE (Pseudocholinesterase)  
GN Name=BChE; Synonyms=CHE1;  
OS Homo sapiens (Human);  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=90212557; PubMed=2322535;  
RA Arpagaus M., Koet M., Vatsis K.F., Bartels C.F., la Du B.N.,  
RA Lockridge O.;  
RT "Structure of the gene for human butyrylcholinesterase. Evidence for a  
RT single copy.";  
RL Biochemistry 29:124-131(1990).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=87231856; PubMed=3035536;  
RA Prody C.A., Zevin-Sonkin D., Gnat A., Goldberg O., Soreq H.;  
RT "Isolation and characterization of full-length cDNA clones coding for  
RT cholinesterase from fetal human tissues.";  
RL Proc. Natl. Acad. Sci. U.S.A. 84:3555-3559(1987).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=86016155; PubMed=3477799;  
RA McIernan C., Adkins S., Chatonnet A., Vaughan T.A., Bartels C.F.,  
RA Koet M., Rosenberry T.L., la Du B.N., Lockridge O.;  
RT "Brain cDNA clone for human cholinesterase.";  
RL Proc. Natl. Acad. Sci. U.S.A. 84:6682-6686(1987).  
RN [4]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22288957; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Uediri T.B., Toshiyuki S., Abramson R.D., Mullaly S.J.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Malek J.A., Gunaratne P.H.,  
RA Bosak S.A., McMan P.J., McKernan K.J., Gay L.J., Hulyk S.W.,  
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Munzy D.M., Sodergren B.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kerteman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butcherfield Y.S.N., Krzywiński M.I., Skalska U.A., Smalins D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marita M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [5]  
RP SEQUENCE OF 29-602.  
RX TISSUE=Plasma;  
RC MEDLINE=87109144; PubMed=3542989;  
RA Lockridge O., Bartels C.F., Vaughan T.A., Wong C.K., Norton S.E.,  
RA Johnson L.L.;  
RT "Complete amino acid sequence of human serum cholinesterase.";  
RL J. Biol. Chem. 262:549-557(1987).  
RN [6]

RP DISULFIDE BONDS.  
RX MEDLINE=88007487; PubMed=1115973;  
RA Lockridge O., Adkins S., la Du B.N.;  
RT "Location of disulfide bonds within the sequence of human serum  
RT cholinesterase.";  
RL J. Biol. Chem. 262:12945-12952(1987).  
RN [7]  
RP REVIEW.  
RX MEDLINE=89149758; PubMed=3067729;  
RA Lockridge O.;  
RT "Structure of human serum cholinesterase.";  
RL Bioessays 9:125-128(1988).  
RN [8]  
RP VARIANT ATYPICAL GLY-98.  
RX MEDLINE=89128896; PubMed=2915989;  
RA McGuire M.C., Nogueira C.P., Bartels C.F., Lightstone H., Hajra A.,  
RA van der Spek A.F.L., Lockridge O., la Du B.N.;  
RT "Identification of the structural mutation responsible for the  
RT dibucaine-resistant (atypical) variant form of human serum  
RT cholinesterase.";  
RL Proc. Natl. Acad. Sci. U.S.A. 86:953-957(1989).  
RN [9]  
RP VARIANT ILE-358.  
RX MEDLINE=96287386; PubMed=8680411;  
RA Iida S., Kinoshita M., Fujii H., Moriyama Y., Nakamura Y., Yura N.,  
RA Moriwa K.;  
RT "Mutations of human butyrylcholinesterase gene in a family with  
RT hypocholesterolemia.";  
RL Hum. Mutat. 6:349-351(1995).  
RN [10]  
RP CARBOLYMIC ACTIVITY: An acylcholine + H(2)O = choline + a  
RP carboxylic acid anion. The tetramer is composed of two dimers. The  
RP two subunits in a dimer are linked by a disulfide bond.  
RP TISSUE SPECIFICITY: Present in most cells except erythrocytes.  
RP DISEASE: Mutant alleles of CHE1 are responsible for  
RP hypocholesterolemia resulting in suxamethonium sensitivity.  
RP Homozygous persons sustain prolonged apnea after administration of  
RP the muscle relaxant suxamethonium in connection with surgical  
RP anesthesia.  
RP MISCELLANEOUS: Cholinesterase is highly reactive with  
RP organophosphate esters.  
RP SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.  
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CC -----  
CC EMBL; M32391; AAA99296.1; JOINED.  
CC EMBL; M32389; AAA99296.1; JOINED.  
CC EMBL; M32390; AAA99296.1; JOINED.  
CC EMBL; M16541; AAA98113.1; --  
CC EMBL; M16474; AAA52015.1; --  
CC EMBL; BC018141; AAH18141.1; --  
CC PIR; A33769; ACHU.  
CC PDB; 1BHQ; Model; A=30-560.  
CC PDB; 1EHQ; Model; A=30-560.  
CC PDB; 1P01; X-ray; A=29-557.  
CC PDB; 1P0M; X-ray; A=29-557.  
CC PDB; 1P0P; X-ray; A=29-557.  
CC PDB; 1P0Q; X-ray; A=29-557.  
CC GeneW; HGNC; 983; BChE.  
CC MIM; 177400; --  
CC GO; GO:0001540; F:beta-amyloid binding; NMS.  
CC GO; GO:0003824; F:catalytic activity; NMS.  
CC GO; GO:0004104; F:cholinesterase activity; NMS.  
CC GO; GO:0004989; F:enzyme binding; NMS.  
CC GO; GO:0050783; P:cocaine metabolism; NMS.  
CC InterPro; IPR002018; CarbesteraseB.  
CC InterPro; IPR000997; Cholinesterase.



DR	InterPro: IPR00379; Ser ester.
DR	Pfam: PF0013; Coesterase; 1.
DR	PRINTS; PR00878; CHOLNESTRASE.
DR	PROSITE; PS00122; CARBOXYL ESTERASE B_1; 1.
DR	PROSITE; PS00941; CARBOXYL ESTERASE B_2; 1.
KW	3D-structure; Direct protein sequencing; Disease mutation;
KV	Glycoprotein; Hydrolase; Polymorphism; Serine esterase; Signal.
FT	SIGNAL
FT	CHAIN 1 28
FT	ACT SITE 29 602 Cholinesterase.
FT	ACT SITE 226 226 Acyl-ester intermediate (By similarity).
FT	ACT SITE 353 353 Charge relay system (By similarity).
FT	ACT SITE 466 466 Charge relay system (By similarity).
FT	DISULFID 93 120
FT	DISULFID 280 291
FT	DISULFID 428 547
FT	DISULFID 599 599 Interchain.
FT	CARBOHYD 45 45 N-linked (GlcNAc . . ).
FT	CARBOHYD 85 85 N-linked (GlcNAc . . ).
FT	CARBOHYD 134 134 N-linked (GlcNAc . . ).
FT	CARBOHYD 269 269 N-linked (GlcNAc . . ).
FT	CARBOHYD 284 284 N-linked (GlcNAc . . ).
FT	CARBOHYD 369 369 N-linked (GlcNAc . . ).
FT	CARBOHYD 483 483 N-linked (GlcNAc . . ).
FT	CARBOHYD 509 509 N-linked (GlcNAc . . ).
FT	CARBOHYD 514 514 N-linked (GlcNAc . . ).
FT	VARIANT 98 98 D -> G (in atypical form, dibucaine-resistant; dbSNP:179807).
FT	VARIANT 271 271 /FTId=VAR_002360.
FT	VARIANT 358 358 T -> M (in fluoride-1).
FT	VARIANT 358 358 /FTId=VAR_002361.
FT	VARIANT 418 418 L -> I (in hypocholesterolemia).
FT	VARIANT 418 418 /FTId=VAR_002362.
FT	VARIANT 567 567 G -> V (in fluoride-2).
FT	VARIANT 567 567 /FTId=VAR_002363.
FT	VARIANT 567 567 A -> T (in K variant; with reduced enzyme activity; dbSNP:1803274).
FT	SEQUENCE 602 AA; 68418 MW; C9836409D9057F27 CRC64; /FTId=VAR_002364.
Query Match	99.5%; Score 3096; DB 1; Length 602;
Best Local Similarity	99.8%; Pred. No. 2..3e-224;
Matches 573; Conservative	0; Mismatches 1; Indels 0; Gaps 0
Dy	1 EDDIIATKNGKVGRGNLTIVFGGYTAFLGIYAPPLGRLLPFKKRQSTITKMSDIWNATK 60
Dd	EDDIIATKNGKVGRGNLTIVFGGYTAFLGIYAPPLGRLLPFKKRQSTITKMSDIWNATK 88
Dy	YANSCCONIDOSFPFHSGEMNNPTDTISEDCLYTNVMTPARKPKNATYLTIYGGSPOT 120
Dd	YANSCCONIDOSFPFHSGEMNNPTDTISEDCLYTNVMTPARKPKNATYLTIYGGSPOT 148
Dy	121 GTSSLIHVVDGKFLAVERVIIVSVNMYRGALGFLLPGNPENAPGMNGLFDDQLALQMVK 180
Dd	GTSSLIHVVDGKFLAVERVIIVSVNMYRGALGFLLPGNPENAPGMNGLFDDQLALQMVK 208
Dy	181 NIAAFGPNKSYTLFGESAGAAVSGLHLISPGSHSLFTRAIILQSSEFNAPMAVTSLYEAR 240
Dd	NIAAFGPNKSYTLFGESAGAAVSGLHLISPGSHSLFTRAIILQSSEFNAPMAVTSLYEAR 268
Dy	241 NRTNLIALKLGSRENRETEIKKCLANKPOEILLNEAPVPVPGTPLSVNPGTVNDDELIT 300
Dd	NRTNLIALKLGSRENRETEIKKCLANKPOEILLNEAPVPVPGTPLSVNPGTVNDDELIT 328
Dy	301 DMPDLILEGOFKTKQIILGVNKDGTFMIVYGAGSGSKDNNSITTRKEFOGLKIFFPG 360
Dd	DMPDLILEGOFKTKQIILGVNKDGTFMIVYGAGSGSKDNNSITTRKEFOGLKIFFPG 388
Dy	361 VSEFGKESILPHYTYMDVDQRPENTREALGDVVGDNFCPALBFTKKRSEWGNAFFYY 420
Dd	VSEFGKESILPHYTYMDVDQRPENTREALGDVVGDNFCPALBFTKKRSEWGNAFFYY 448
Dy	421 FEHRSKLPWPBMGWMGYELEFPFGLPLERRDYTTAEELLSIYKRMANPAKYGNP 480

Db	449	FEHSSXKLPWEMGVHGEIEEFVFGJPLERRDNYTKAEK1LSRSIYKRWANFAYGNP	508
Qy	481	NETONNSTSWVEFESTOKYLLTLNTESTRIMTKLRACQCRWTSFPPVULMTGNIDAE	540
Db	509	NETONNSTSWVEFESTOKYLLTLNTESTRIMTKLRACQCRWTSFPPVULMTGNIDAE	568
Qy	541	WEWAGFHRMNNYMDWKNQCFNDYTSKESCVGL	574
Db	569	WEWAGFHRMNNYMDWKNQCFNDYTSKESCVGL	602

RESULT 2

CHLE_RABIT	STANDARD	ERT	581 AA.
AC	P21927		
DT	01-MAY-1991 (Rel. 18, Created)		
DT	01-MAY-1991 (Rel. 18, Last sequence update)		
DT	01-OCT-2004 (Rel. 45, Last annotation update)		
DE	Cholinesterase precursor (EC 3.1.1.8) (Acylcholine acylhydrolase)		
DE	(Choline esterase II) (Butyrylcholine esterase)		
DE	(Pseudocholinesterase).		
GN	Name=BChE;		
OS	Oryctolagus cuniculus (Rabbit).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.		
OX	NCBI_TaxID=9986;		
RC	SEQUENCE FROM N.A.		
RC	STRAIN=New Zealand;		
RX	MEDLINE=90326526; PubMed=2374720;		
RT	Jbilo O., Roudani S., Chatomnet A.;		
RT	"Complete sequence of rabbit butyrylcholinesterase.";		
RL	Nucleic Acids Res. 18:3990-3990(1990).		
RP	SEQUENCE OF 75-215 FROM N.A.		
RP	TISSUE=Liver;		
RX	MEDLINE=91201348; PubMed=2016308;		
RA	Arpagaus M., Chatomnet A., Maeson P., Newton M., Vaughan T.A.,		
RA	Bartels C.F., Nogueira C.P., La Du B.N., Lockridge O.;		
RT	"Use of the polymerase chain reaction for homology probing of		
RT	butyrylcholinesterase from several vertebrates.";		
RL	J. Biol. Chem. 266:6966-6974(1991).		
CC	-I- CATALYTIC ACTIVITY: An acylcholine + H(2)O = choline + a		
CC	carboxylic acid anion.		
CC	-I- SUBUNIT: Homotetramer. The tetramer is composed of two dimers. The		
CC	two subunits in a dimer are linked by a disulfide bond.		
CC	-I- TISSUE SPECIFICITY: Present in most cells except erythrocytes.		
CC	-I- MISCELLANEOUS: Cholinesterase is highly reactive with		
CC	organophosphate esters.		
CC	-I- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.		
CC	-----		
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CC	or send an email to <a href="mailto:license@ab-sib.ch">license@ab-sib.ch</a> .		
CC	-----		
DR	EMBL; X52090; CAA36308.1; -		
DR	EMBL; X52091; CAA36308.1; JOINED.		
DR	EMBL; X52092; CAA36308.1; JOINED.		
DR	EMBL; M62779; AAA31169.1; -		
DR	PIR; S10255; C39768.		
DR	HSSP; P22303; 1FBU.		
DR	InterPro; IPR002019; CarbesteraseB.		
DR	InterPro; IPR000997; Cholinesterase.		
DR	InterPro; IPR000379; Ser esttr.		
DR	Pfam; PF00135; Coesterase.1.		
DR	PRINTS; PRO0878; CHOLNSTRASE.		
DR	PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.		
DR	PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.		
DR	Glycoprotein;Hydrolase; Serine esterase; Signal.		

FT	SIGNAL	1	8	Potential.
FT	CHAIN	9	581	Cholinesterase.
FT	ACT_SITE	205	205	Acyl-ester intermediate (By similarity).
FT	ACT_SITE	332	332	Charge relay system (By similarity).
FT	ACT_SITE	445	445	Charge relay system (By similarity).
FT	DISULFID	72	99	By similarity.
FT	DISULFID	259	270	By similarity.
FT	DISULFID	407	526	By similarity.
FT	DISULFID	578	578	Interchain (By similarity).
FT	CARBOXYD	64	64	N-linked (GlcNAc . . .) (Potential).
FT	CARBOXYD	113	113	N-linked (GlcNAc . . .) (Potential).
FT	CARBOXYD	248	248	N-linked (GlcNAc . . .) (Potential).
FT	CARBOXYD	263	263	N-linked (GlcNAc . . .) (Potential).
FT	CARBOXYD	348	348	N-linked (GlcNAc . . .) (Potential).
FT	CARBOXYD	462	462	N-linked (GlcNAc . . .) (Potential).
FT	CARBOXYD	488	488	N-linked (GlcNAc . . .) (Potential).
FT	CARBOXYD	492	492	N-linked (GlcNAc . . .) (Potential).
FT	CARBOXYD	493	493	N-linked (GlcNAc . . .) (Potential).
FT	CARBOXYD	581 AA;	66156 MM;	FEED199EF7B32EB0A CRC64;

Query Match	91.4%	Score 2843;	DB 1;	Length 581;
Best Local Similarity	92.0%	Pred. No. 2,4e-205;		
Matches 526; Conservative	12;	Mismatches 34;	Indels 0;	Gaps 0

QY	2	DDIIITATKNGKRGNNILVFGGTWTAIFGI	PYAOPPLGRLRKPKQSLTKMSDINMATX	61
Db	9	EDVILITTKNGRGINLVPFGGIVTAFGLI	PIAOPPLGLRLRKPKQSLTKMSDINMATX	68
QY	62	ANSCCONIDQSPFGFGSEMMNPNTDLS	EDCIYANWIDAPKPKATVLIWYGGGFGQT	121
Db	69	ANSCCONIDQSPFGFGSEMMNPNTDLS	EDCIYANWIDAPKPKATVLIWYGGGFGQT	128
QY	122	TSSLHYTDGKFLARVRVTVSMNTRVGL	ALPGNEAQQNGMLPFOOLALQWVQK	181
Db	129	TSSLQYTDGKFLTRVRVTVSMNTRVGL	ALPGNEAQQNGMLPFOOLALQWVQK	188
QY	182	IAAFGNGPKSVTLFGESAGAASVLIHL	SPGSHSLFTTRAIIQSGSFNAFWATSLYEAN	241
Db	189	IAAFGNGPKSVTLFGESAGAASVLIHL	SPGSHSLFTTRAIIQSGSFNAFWATSLYEAN	248
QY	242	RTLTNAKLTGCSRENTETIIKCLRNDD	POEILINAEFVVPYGRPLSVNGPTVDGFLND	301
Db	249	RTLTNAKLPFGCSTENETETIIKCLRNDD	AOEILINAEFVVPFDLSLVNGPTVDGFLND	308
QY	302	MPDIILELCQFKTQILVGNKDEGTWFL	LYGAGPGFSKDNNSIITRKEPQGLKIFPPGV	351
Db	309	MPDTTLQLOLKTQILVGNKDEGTAF	LYGAGPGFSKDNNSIITRKEPQGLKIFPPGV	358
QY	362	SEFGKESILFHTYDWDQRPENYTRRAL	GVNDVNPICGLAEFTTKFSMGNNAPFTYE	421
Db	369	SEFGKESILFHTYDWDQRPENYTRRAL	DVDVGNPFCGLAEFTTKFSMGNNAPFTYE	428
QY	422	EHHSSKLPMPENMGVNHGYEIEFVFG	PLERRDNYTAAEILSRSIYKRWANPAKYGNPN	481
Db	429	EHHSSKLPMPENMGVNHGYEIEFVFG	PLERRVNYTAAEILSRSIYKRWANPAKYGNPN	488
QY	482	ETONNSTSWPFSYKSTBOKYLTLNTES	TRITKLRACQCRWTSFPFVYLTMTGNIDEAEW	541
Db	489	GTONNSTSWPFSYKSTBOKYLTLNTES	TRITKLRACQCRWTLFPFVLTMTGNIDEAEQ	548
QY	542	EMKAGFHRNNYMMDMKQFNDDYTSKKE	SCVWG 573	
Db	549	EMKAGFHRNNYMMAMKQHNDDYTSKKE	RQCG 580	
RESULT 3				
ID	Q9NIN9	PRELIMINARY;		
AC	Q9NIN9;	PRT; 602 AA.		
DT	01-OCT-2000	(Tremblrel. 15. Created)		
DT	01-OCT-2000	(Tremblrel. 15. Last sequence update)		
DT	01-OCT-2003	(Tremblrel. 25. Last annotation update)		
DE	Butyrylcholinesterase (EC 3.1.1.8).			

GN Name=BCHH;  
OS Equus caballus (Horse).  
OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euteria; Perissodactyla; Equidae; Equus.  
NCBI\_TaxId=9796;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE=20181263; PubMed=10718335;  
RX Wierl M., Morton C.L., Danks M.K., Potter P.M.;  
RT "Isolation and characterization of a cDNA encoding a horse liver  
RT butyrylcholinesterase: evidence for CPr-11 drug activation.";  
RL Biochem. Pharmacol. 59:773-781 (2000).  
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/Lipase family.  
EMBL AF178685; AAF61480.1' -.  
DR HSSP; P21836; INSM.  
DR GO; GO:0004104; F:cholinesterase activity; IEA.  
DR GO; GO:0016787; F:hydrolase activity; IEA.  
DR InterPro; IPR002018; Carboxylestab.  
DR InterPro; IPR000997; Cholinesterase.  
DR InterPro; IPR000379; Ser\_cattr.  
DR Pfam; PF00135; Coesterase; 1.  
DR PRINTS; PR00878; CHOLINESTRASE.  
DR PROSITE; PS00122; CARBOXYLESTERASE\_B\_1; 1.  
DR PROSITE; PS00941; CARBOXYLESTERASE\_B\_2; 1.  
KM Hydrolase.  
SQ SEQUENCE 602 AA; 68838 MW; 94c73P00431DF25E CRC64;

Query Match	99.2%;	Score 2775;	DB 2;	Length 602;
Best Local Similarity	80.4%;	Pred. No. 3.4e-270;		
Matches 518;	Conservative 19;	Mismatches 34;	Indels 0;	Gaps 0

Qy	1	EDDIIATKNGKVKRGMNLTVBGGITVATLGIPIYAOPRLGSLRPFKPKPSLTAKMSDINMANK	60
Db	29	EEBIIITTTNGKRGKGNLPLVGLGITVATLGIPIYAOPRLGSLRPFKPKPSLTAKMSINMANK	88
Qy	61	YANSCCONIDQSPFGHFGHEMMNPNTDLSBDCLYLAWMIWPAKPKNATVLIWYGAGFOT	120
Db	89	YANSCYQNDQSPFGPLGSEMMNPNTLSEDCLYLAWMIWPAKPKNATVMIWYGGGFOT	148
Qy	121	GTSSLHAYDOKFLARERIVYVSNMYRGAIGFLALPGNPAAPGNMGLPFOOLALOMVOK	180
Db	149	GTSSLPAYDOKFLARERIVYVSNMYRGAIGFLALSNPAPAGNMGLPFOOLALOMVOK	208
Qy	181	NIAAFGNPFSVTLFPGESAGASVSILHLSPGSHSLFTRAILQSGSFNAFMAVTSLEYAR	240
Db	209	NIAAFGNPFSVTLFPGESAGASVSILHLSPRSPOLFTRAILQSGSSNAFMAVTSLEYAR	268
Qy	241	NRTNLIAKLGCGRNETHETIKCLRNKQPOEILNEAFVYVGYGPIPLSVNGPTVDGFLT	300
Db	269	NRTLLIAKRNKGRNETHETIKCLRNKQPOEILNEAFVYVGYGPIPLSVNGPTVDGFLT	328
Qy	301	DMPDILLIQPFKTOILVGNKDKBGTWLVLYGAFGRSKNNSTIITREPOEGLKIFPG	360
Db	329	DMPDTLLIQPFKTOILVGNKDKBETALVYGAGFSKNNSTIITREPOEGLKIFPR	388
Qy	361	VSEPGKESILFPHYTDWDDQRPENYEAALGDVAVGYNELCPALBETKFKSEMGNNAEFY	420
Db	389	VSEGRGKESILFHYTMDLDDQRAENYEAALDVAVGYNIIICPALBETKFKSELGNDAAEFY	448
Qy	421	FEHRSSKILPMEPMWGVNWHGEIEIFVGLGLEPRDNYTAABELLSIYKRWANPAKGNP	480
Db	449	FEHRSTKILPMEPMWGVNWHGEIEIFVGLGLEPRVYTAABELLSIYKRWANPAKGNP	508
Qy	481	NETQNNSTWSPVEFKSTEQKYLINTSTSTIMTKLRAOQCRFWTSEFPVLEMTGNIDAE	540
Db	509	NETQNSNTRWVFEKSTEQKYLINTSPSKYIKTLRAOQCRFWTLFFPVLEMTGNIDAE	568
Qy	541	WEKAGFHRANNNYMDKQNPNDYTSKSSC	571
Db	569	WEKAGFHRANNNYMDKQNPNDYTSKSSC	599

## RESULT 4

CHLE\_HORSE  
ID CHLE\_HORSE STANDARD; PRT; 574 AA.  
AC P81908;  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 01-OCT-2004 (Rel. 45, Last annotation update)  
DE Cholinesterase (EC 3.1.1.8) (Acylcholine acylhydrolase) (Choline  
esterase II) (Butyrylcholine esterase) (Pseudocholinesterase) (Eo-  
BCH)  
GN Name=BCH;  
OS Equus caballus (Horse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
OX NCBI\_TaxID=9796;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Plasma;  
RA Moored D.R., Luo C., Garcia G.E., Doctor B.P.;  
RT "Amino acid sequence of horse serum butyrylcholinesterase."  
RL (In) Doctor B.P., Taylor P., Quinn D.M., Rotundo R.L., Gentry M.K.  
(eds.);  
RL Structure and function of cholinesterases and related proteins,  
pp.145-146, Plenum Press, New York and London (1998).  
CC -1- CATALYTIC ACTIVITY: An acylcholine + H(2)O = choline + a  
carboxylic acid anion.  
CC -1- SUBUNIT: Homotetramer. The tetramer is composed of two dimers. The  
two subunits in a dimer are linked by a disulfide bond.  
CC -1- TISSUE SPECIFICITY: Present in most cells except erythrocytes.  
CC -1- MISCELLANEOUS: Cholinesterase is highly reactive with  
organophosphate esters.  
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.  
DR HSSP; P21836; INSM.  
DR InterPro; IPR002018; Carboxylesterase.  
DR InterPro; IPR000997; Cholinesterase.  
DR InterPro; IPR000379; Ser\_estrs.  
DR Pfam; PF00135; Coesterase; 1.  
DR PRINTS; PR00878; CHOLINESTRASE.  
DR PROSITE; PS00122; CARBOXYLESTERASE\_B\_1; 1.  
DR PROSITE; PS00941; CARBOXYLESTERASE\_B\_2; 1.  
KW Direct protein sequencing; Glycoprotein; Hydrolase; Serine esterase.  
FT ACT\_SITE 198 198 Acyl-ester intermediate (By similarity).  
FT ACT\_SITE 325 325 Charge relay system (By similarity).  
FT ACT\_SITE 438 438 Charge relay system (By similarity).  
FT DISULFID 65 92 By similarity.  
FT DISULFID 252 263 By similarity.  
FT DISULFID 400 519 By similarity.  
FT DISULFID 571 571 Interchain (By similarity).  
FT CARBOHYD 57 57 N-linked (G1cNAc...).  
FT CARBOHYD 106 106 N-linked (G1cNAc...).  
FT CARBOHYD 241 241 N-linked (G1cNAc...).  
FT CARBOHYD 256 256 N-linked (G1cNAc...).  
FT CARBOHYD 341 341 N-linked (G1cNAc...).  
FT CARBOHYD 455 455 N-linked (G1cNAc...).  
FT CARBOHYD 481 481 N-linked (G1cNAc...).  
FT CARBOHYD 486 486 N-linked (G1cNAc...).  
SQ SEQUENCE 574 AA; 65641 MW; 07755EB9FB9CB33E CMC64;  
Query Match 89.2%; Score 2774; DB 1; Length 574;  
Best Local Similarity 90.5%; Pred. No. 3.8e-200;  
Matches 517; Conservative 20; Mismatches 34; Indels 0; Gaps 0;

QY 181 NIAAFGNPKSVTLFGESAGASVSLHLSPGSHSLFTRAILDGGSPNAPWATSLYEAR 240  
DB 181 NIAAFGNPKSVTLFGESAGASVSLHLSPGSHSLFTRAILDGGSPNAPWATSLYEAR 240  
QY 241 NRTLNIAKLKGCGRNTEIILKLRNMDPOEIIILNEAFVYPCPTPLSVNPGPTDGGFLT 300  
DB 241 NRTLNIAKLKGCGRNTEIILKLRNMDPOEIIILNEAFVYPCPTPLSVNPGPTDGGFLT 300  
QY 301 DMPDILLEGQPKKQTLIVGNKDEGTWFLVYGAAPGSKDNNSIITKEFOEGIKTFPPG 360  
DB 301 DMPDILLEGQPKKQTLIVGNKDEGTWFLVYGAAPGSKDNNSIITKEFOEGIKTFPPG 360  
QY 361 VSEFGKSIIFHYTDWDDRPENYRALGDVVDYVFCPALFETKSEKGNNAFFY 420  
DB 361 VSEFGKSIIFHYTDWDDRPENYRALGDVVDYVFCPALFETKSEKGNNAFFY 420  
QY 421 FEHRSSKLPPEPMGWVGHGIEFFVGLPLERRVNTYRAEIIISRSIMKMANFAKYNP 480  
DB 421 FEHRSSKLPPEPMGWVGHGIEFFVGLPLERRVNTYRAEIIISRSIMKMANFAKYNP 480  
QY 481 NETQNNSTSWVPFSTQKTLTNTSESTRIMTKLRBAQCFMTSPFKVLEMTGNDIEAE 540  
DB 481 NETQNNSTSWVPFSTQKTLTNTSESTRIMTKLRBAQCFMTSPFKVLEMTGNDIEAE 540  
QY 541 MEWKAQFHRNNYMMDMKQFNNDYTSKESG 571  
DB 541 MEWKAQFHRNNYMMDMKQFNNDYTSKESG 571

RESULT 5

CHLE\_FELCA  
ID CHLE\_FELCA STANDARD; PRT; 602 AA.  
AC 062760;  
DT 29-MAR-2004 (Rel. 43, Last sequence update)  
DT 29-MAR-2004 (Rel. 43, Last sequence update)  
DT 01-OCT-2004 (Rel. 45, Last annotation update)  
DE Cholinesterase precursor (EC 3.1.1.8) (Acylcholine acylhydrolase)  
DE (Choline esterase II) (Butyrylcholine esterase)  
GN Name=BCH;  
OS Felis silvestris catus (Cat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
OX NCBI\_TaxID=9685;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Pituitary;  
RA MEDLINE=20334351; PubMed=10874122;  
RA Bartels C.F., Xie W., Miller-Lindholm A.K., Schopfer L.M.,  
RA Lockridge O.;  
RT "Determination of the DNA sequences of acetylcholinesterase and  
butyrylcholinesterase from cat and demonstration of the existence of  
both in cat plasma."  
RL Biochem. Pharmacol. 60:479-487(2000).  
CC -1- CATALYTIC ACTIVITY: An acylcholine + H(2)O = choline + a  
carboxylic acid anion.  
CC -1- SUBUNIT: Homotetramer. The tetramer is composed of two dimers. The  
two subunits in a dimer are linked by a disulfide bond (By  
similarity).  
CC -1- MISCELLANEOUS: Cholinesterase is highly reactive with  
organophosphate esters (By similarity).  
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
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entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC EMBL; AF053483; AAC06261.1; -.  
DR HSSP; P22303; IB41.

	DR	InterPro:	IPR002018;	CarbesteraseB.
	DR	InterPro:	IPIR00097,	Cholinesterase.
	DR	InterPro:	IPIR00379;	Ser est.
	DR	Pfam:	PF00135;	Coesterase_1.
	DR	PRINTS:	PRO0678;	CHOLINESTRASE.
	DR	PROSITE:	PS00122;	CARBOXYLESTERAS_B_1; 1.
	DR	PROSITE:	PS00941;	CARBOXYLESTERAS_B_2; 1.
KM		Glycoprotein:	Hydrolase;	Serine esterase; Signal.
FT	SIGNAL		1	28 Potential.
FT	CHAIN		29	602 Cholinesterase.
FT	ACT_SITE		226	226 Acyl-ester intermediate (By similarity).
FT	ACT_SITE		353	353 Charge relay system (By similarity).
FT	ACT_SITE		466	466 Charge relay system (By similarity).
FT	DISULFD		93	120 By similarity.
FT	DISULFD		280	291 By similarity.
FT	DISULFD		428	547 By similarity.
FT	DISULFD		599	599 Interchain (By similarity).
FT	CARBOHYD		85	85 N-linked (GlcNAc... ) (Potential).
FT	CARBOHYD		134	134 N-linked (GlcNAc... ) (Potential).
FT	CARBOHYD		269	269 N-linked (GlcNAc... ) (Potential).
FT	CARBOHYD		284	284 N-linked (GlcNAc... ) (Potential).
FT	CARBOHYD		369	369 N-linked (GlcNAc... ) (Potential).
FT	CARBOHYD		483	483 N-linked (GlcNAc... ) (Potential).
FT	CARBOHYD		509	509 N-linked (GlcNAc... ) (Potential).
FT	CARBOHYD		513	513 N-linked (GlcNAc... ) (Potential).
FT	CARBOHYD		514	514 N-linked (GlcNAc... ) (Potential).
SEQ	SEQUENCE		602 AA;	68328 MW; EC08079232B7AB9C CR64;

Query Match	Score 2696;	DB 1;	length 603;
Best Local Similarity	87.6%;	Pred. No. 3e-194;	
Matches 503;	Conservative 2;	Mismatches 49;	Indels 0;
			Gaps 0;

```

0Y      1 EBDIIIAIKNGVVRKGNLTVFGJIVAFAGIYADPEBRLKRFKQSLIANSIDIMAKN 30
Db      29 EBDIIITTKNGKVRGNLTVLDIGVTAFIGIYPADPGLRLFKKKQPLTKMSDIMNAK  88
0Y      61 YANSCCQNDIGSFPFGHSEMMNPMTDISEDCLYINWVTPARKPNATYLIYGGSGFOT 120
Db      89 YANSCYQVADDSFGPGHSEMMNPMTDISEDCLYINWVTPRKPNATYMIYGGSGFOT 148
0Y      121 GTSLSHYVDGKFLARVERIYVSMYRVGALGFIALPGNPEARGNGLFDQDLALQWYK 180
Db      149 GTSLSPEYDQKFLARVERIYVSMYRVGALGFIALPGNPEYRGNGGLFDQDLALQWYK 208
0Y      181 NIAAFGNKSVYTLFGESAGAAVSLSHLSPGSHLFTRAIIQSGSFNAPAVTSIYEAR 240
Db      209 NIAARGNKSJTLFGESAGASVSLHLLSPRSQPLFTRAIIQSGSSNAPMAVMSIDEAK 268
0Y      241 NRTLIATKLTCGSGRENETETIKCLRKKNDPOEILINAFVVPYCTPLSVNFGPVODFILT 300
Db      269 NRTLIATKLTCGSKENDTETIKCLRKKNDPOEILINLVLVPSDTLTSVNFPGVVDDEFLT 328
0Y      301 DMPDILLETIGQPKKQIILGVNNDSEGTWFLVYGAPGFSKDNNSITRKFEQEGKLTFPG 360
Db      329 DMPDITLQIGQPKKQIILGVNNDSEGTAFIVGAPGFSKDNNSITRKFEQEGKLTFPG 388
0Y      361 VSBFGKESIIFHYTDWDDQRPENYREALGDVVDNYFLCPALFTTKTSEWGNAFFYY 420
Db      389 VSBFGKHALIFLYVDLDDQRAKRYEALDDVGDVNIICPALFPTTKSELGNNAFFYY 448
0Y      421 FEHRSSKLPWPEMVGWGHGIEFVGLPIERRDNTYKAEIISRSIYKMANPAKYGNP 480
Db      449 FEHRSSQLPPEMVGWGHGIEFVGLPIERRVNTYRAEIIISRSIYMANPAKYGNP 508
0Y      481 NETQNNSTSWPVFKSTJEOKYLITNTSSTRIMTLKRAQOCCFWWSFPKYLEMNGNIDEAE 540
Db      509 NGTQNNSTWPAFRSDIOKYLITNABSPKYTKLRQOCCFWTLFPKYLEMNGNIDEAE 568
0Y      541 WEKAGSHRNNNTMMQKNOFNQYTSKESCVGL 574
Db      569 WEKAGSHRNNNTMMQKNOFNQYTSKESCVGL 602

```

RESULT 6	
CHLE_PANTT	
ID _CHLE_PANTT	STANDARD;
	PRT;
	602 AA

DT	29-MAR-2004 (Rel. 43, Last sequence update)
DT	29-MAR-2004 (Rel. 43, Last annotation update)
DT	01-OCT-2004 (Rel. 45, Last annotation update)
DE	Cholinesterase precursor (EC 3.1.1.8) (Acetylcholine acylhydrolase)
DE	(Choline esterase II) (Butyrylcholine esterase)
DE	(Pseudocholinesterase).
GN	Name=BCHr;
OS	Panthera tigris tigris (Bengal tiger).
OC	Eukaryota; Metazoa; Chordata; Carnivora; Fissipedia; Felidae; Panthera.
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Panthera.
OX	NCBI_TaxID=74535;
RN	(1)
RP	SEQUENCE FROM N.A.
RC	TISSUE=Plutalry;
RX	MEDLINE=20334351; PubMed=10874122;
RA	Bateis C.F., Xie W., Miller-Jindholm A.K., Schopfer L.M.,
RA	Lockridge O.;
RT	"Determination of the DNA sequences of acetylcholinesterase and
RT	butyrylcholinesterase from cat and demonstration of the existence of
RL	both in cat plasma."
RT	Biochem. Pharmacol. 60:479-487(2000).
CC	-1 CATALYTIC ACTIVITY: An acylcholine + H(2)O = choline + a
CC	carboxylic acid anion.
CC	-1 SUBUNIT: Homotetramer. The tetramer is composed of two dimers. The
CC	two subunits in a dimer are linked by a disulfide bond (By
CC	similarity).
CC	-1 MISCELLANEOUS: Cholinesterase is highly reactive with
CC	organophosphate esters (By similarity).
CC	-1 SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC	entities requires a license agreement (See <a href="http://www.isb-sb.ch/announce/">http://www.isb-sb.ch/announce/</a>
CC	or send an email to <a href="mailto:license@isb-sb.ch">license@isb-sb.ch</a> ).
CC	-----
DR	EMBL; AF053484; AAC06262.1; -
DR	HSSP; P22303; 1B41.
DR	InterPro: IPR002018; Carbesteraseb.
DR	InterPro: IPR000397; Cholinesterase.
DR	InterPro: IPR003379; Ser estase.
DR	Pfam; PF00135; Coesterasec.1
DR	PRINTS; PR00878; CHOLINESTRASE.
DR	PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR	PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW	Glycoprotein; Hydrolase; Serine esterase; Signal.
FT	SIGNAL 1 28
FT	CHAIN 29 602
FT	ACT_SITE 226 226
FT	ACT_SITE 353 353
FT	ACT_SITE 466 466
FT	DISULFID 93 120
FT	DISULFID 280 291
FT	DISULFID 547 547
FT	DISULFID 599 599
FT	CARBOHYD 85 85
FT	CARBOHYD 134 134
FT	CARBOHYD 269 269
FT	CARBOHYD 284 284
FT	CARBOHYD 369 369
FT	CARBOHYD 483 483
FT	CARBOHYD 509 509
FT	CARBOHYD 513 513
FT	CARBOHYD 514 514
SO	SEQUENCE 602 AA; 68289 MW; EB0C8B9148E956A1 CRC64;

Best Local Similarity 87.3%; Pred. No. 2.4e-193;  
Matches 501; Conservative 23; Mismatches 50; Indels 0; Gaps 0;

QY 1 EDDIIITKNGKVGAMLVFGGVTATAGIPIYAOPPLGRLRFKKKPOSLTKMSDINATK 60  
D 29 EBDIIITTKNGKVGAMLVFGGVTATAGIPIYAOPPLGRLRFKKKPOSLTKMSDINATK 88  
QY 61 YANSCCONIDQSPFGFSGEMMNPTDLSBDCLYLWVWIPAPKPKATVLIWYGGGFO 120  
D 89 HANSCYQNAQDSFGFPGSEMMNPTDLSBDCLYLWVWIPAPKPKATVLIWYGGGFO 148  
QY 121 GTSSLHYDGGKFLARVERVIVSMNRYGALGFLALPBNPAPGNGMGLFDOOLALQWY 180  
D 149 GTSSLHYDGGKFLARVERVIVSMNRYGALGFLALPBNPAPGNGMGLFDOOLALQWY 208  
QY 181 NIAAFGNPKSVTLFGSAGASVSLHLSGSHSLFTRAILQSGSPAPAVSLYEAR 240  
D 209 NIAAFGNPKSVTLFGSAGASVSLHLSGSHSLFTRAILQSGSPAPAVSLYEAR 268  
QY 241 NRTTLAKLTGSRNENETIICKLRNKPDEILNEAFVYGTPLSVNFGPTVDGFLT 300  
D 269 NRTTLAKLTGSRNENETIICKLRNKPDEILNEAFVYGTPLSVNFGPTVDGFLT 328  
QY 301 DMPDILLBLGQFKTKQILVGNKDEGTWFLVYGAPGSKDNNSITTRKEFOGLKIFPG 360  
D 329 DMPDILLBLGQFKTKQILVGNKDEGTWFLVYGAPGSKDNNSITTRKEFOGLKIFPG 388  
QY 361 VSESGKSLIFHYDWDVDDORPENYREALGDVNDVNPICALEFTKFSWGNAPRY 420  
D 389 VSESGKSLIFHYDWDVDDORPENYREALGDVNDVNPICALEFTKFSWGNAPRY 448  
QY 421 FEHSSKLPMPWEMVGHVIEFVGLPLERDNYTAEIISRYIKRANFATYGNP 480  
D 449 FEHSSKLPMPWEMVGHVIEFVGLPLERDNYTAEIISRYIKRANFATYGNP 508  
QY 481 NETONNSTWPFKSTOKYTLTTESTRTMTKLRPAQOCRFWTSPPKVLMTGNIDAE 540  
D 509 NGTONNSTWPFKSTOKYTLTTESTRTMTKLRPAQOCRFWTSPPKVLMTGNIDAE 568  
QY 541 WEKAGFHRMNMVMDKNOFNQDTSKESCVGL 574  
D 569 WEKAGFHRMNMVMDKNOFNQDTSKESCVGL 602

RESULT 7  
BAC34196 PRELIMINARY; PRT; 603 AA.  
AC BAC34196;  
DT 14-APR-2004 (TREMBlrel. 27, Created)  
DT 14-APR-2004 (TREMBlrel. 27, Last sequence update)  
DT 14-APR-2004 (TREMBlrel. 27, Last annotation update)  
DE Adult male liver tumor cDNA, RIKEN full-length enriched library,  
DS clone: C730033G20 product: butyrylcholinesterase.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Liver;  
RX MEDLINE=22354683; PubMed=12466851;  
RA The RIKEN Consortium,  
RA The RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs."  
RL Nature 420:563-573 (2002).  
RP [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Liver;  
RX MEDLINE=21085660; PubMed=11217851;  
RA RIKEN PANTOM Consortium;  
RT "Functional annotation of a full-length mouse cDNA collection."  
RL Nature 409:685-690 (2001).

RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Liver;  
RX MEDLINE=99279253; PubMed=10349636;  
RA Carninci P., Hayashizaki Y.,  
RT "High-efficiency full-length cDNA cloning."  
RL Mech. Enzymol. 303:19-44 (1999).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Liver;  
RX MEDLINE=20499374; PubMed=11042159;  
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.,  
RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
RT prepare full-length cDNA libraries for rapid discovery of new genes."  
RL Genome Res. 10:1617-1630 (2000).  
RN [5]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Liver;  
RX MEDLINE=20530913; PubMed=11076861;  
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
RA Kono H., Akiyama J., Nishi K., Kikunai T., Tashiro H., Itoh M.,  
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,  
RA Okazaki Y., Ishikawa T., Ozawa K., Tanaka T., Matsumura S., Kawai J.,  
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,  
RT "RIKEN integrated sequence analysis (RISA) system-384-format  
RT sequencing pipeline with 384 multicapillary sequencer."  
RL Genome Res. 10:1757-1771 (2000).  
RN [6]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Liver;  
RX MEDLINE=20530913; PubMed=11076861;  
RA Aichi J., Aizawa K., Akiyama J., Arakawa T., Bono H., Carninci P.,  
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
RA Hayashizaki K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,  
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,  
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohnato N., Okazaki Y.,  
RA Saito R., Satoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,  
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,  
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AK050337; BAC34196.1; 2CB79C46797B3713 CRC64;  
SQ SEQUENCE 603 AA; 68462 MW; 2CB79C46797B3713 CRC64;  
Query Match 81.4%; Score 2530; DB 2; Length 603;  
Best Local Similarity 80.7%; Pred. No. 9.6e-182;  
Matches 463; Conservative 47; Mismatches 64; Indels 0; Gaps 0;

QY 1 EDDIIITKNGKVGAMLVFGGVTATAGIPIYAOPPLGRLRFKKKPOSLTKMSDINATK 60  
D 29 EBDIIITTKNGKVGAMLVFGGVTATAGIPIYAOPPLGRLRFKKKPOSLTKMSDINATK 88  
QY 61 YANSCCONIDQSPFGFSGEMMNPTDLSBDCLYLWVWIPAPKPKATVLIWYGGGFO 120  
D 89 HANSCYQNAQDSFGFPGSEMMNPTDLSBDCLYLWVWIPAPKPKATVLIWYGGGFO 148  
QY 121 GTSSLHYDGGKFLARVERVIVSMNRYGALGFLALPBNPAPGNGMGLFDOOLALQWY 180  
D 149 GTSSLHYDGGKFLARVERVIVSMNRYGALGFLALPBNPAPGNGMGLFDOOLALQWY 208  
QY 181 NIAAFGNPKSVTLFGSAGASVSLHLSGSHSLFTRAILQSGSPAPAVSLYEAR 240  
D 209 NIAAFGNPKSVTLFGSAGASVSLHLSGSHSLFTRAILQSGSPAPAVSLYEAR 268  
QY 241 NRTTLAKLTGSRNENETIICKLRNKPDEILNEAFVYGTPLSVNFGPTVDGFLT 300  
D 269 NRTTLAKLTGSRNENETIICKLRNKPDEILNEAFVYGTPLSVNFGPTVDGFLT 328  
QY 301 DMPDILLBLGQFKTKQILVGNKDEGTWFLVYGAPGSKDNNSITTRKEFOGLKIFPG 360

DB 330 DMHTLLQGLKVKKAQILVGVNDGEGAFVYGAPEPSKDNLSLIRKKEFGSLNNYFPG 389  
 QY 361 VSEFGESEILFHTDWDDORPENYREALGDVVDNFCIPALEFTKSEWGNNAFFY 420  
 DB 390 VSLRGEAVLFYVDWGEQSPVYDADVDVGDNIICPALEFTKRAELENNAFFY 449  
 QY 421 FEHRSSKLPWPEWGVHGYEIEFVGLPLERRDNTYKAEILSRIVKMANFAKYGNP 480  
 DB 450 FEHRSSKLPWPEWGVHGYEIEFVGLPLERRDNTYKAEILSRIVKMANFAKYGNP 509  
 QY 481 NETONNSTSPVPEKSTOKTLTNTSTRIMTLRAQOGRFMTSPFKYLEMNGINDAE 540  
 DB 510 NGTQGNSTWMPVFTSTOKTLTNTSTRIMTLRAQOGRFMTSPFKYLEMNGINDAE 569  
 QY 541 WEMKAGFHRNNYMMDMKQNFNDYTSKESCVGL 574  
 DB 570 QEMKAGFHRNNYMMDMKQNFNDYTSKESCVGL 603

RESULT 8

CHLE\_MOUSE STANDARD; PRT; 603 AA.

AC Q0331; 01-OCT-1993 (Rel. 27, Created)  
 DT 01-OCT-1993 (Rel. 27, Last sequence update)  
 DT 01-OCT-2004 (Rel. 45, Last annotation update)  
 DE Cholinesterase precursor (EC 3.1.1.8) (Acylcholine acylhydrolase)  
 DE (Choline esterase II) (Butyrylcholine esterase)  
 DE (Pseudocholesterase)  
 GN Name=Behe;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OC NCBI\_Taxid=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90380429; PubMed=2400605;  
 RA Rachtinsky T.L., Camp S., Li Y., Ekstrom T.J., Newton M., Taylor P.;  
 RT "Molecular cloning of mouse acetylcholinesterase: tissue distribution  
 of alternatively spliced mRNA species";  
 RL Neuron 5:317-327(1990).  
 RN [2]  
 RP SEQUENCE OF 97-237 FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=91201148; PubMed=2016308;  
 RA Arpagaus M., Chaconet A., Masson P., Newton M., Vaughan T.A.,  
 RA Barrels C.F., Nogueira C.P., La Du B.N., Lockridge O.;  
 RT "Use of the polymerase chain reaction for homology probing of  
 butyrylcholinesterase from several vertebrates";  
 RL J. Biol. Chem. 266:6966-6974(1991).  
 CC -1- CATALYTIC ACTIVITY: An acylcholine + H(2)O = choline + a  
 carboxylic acid anion.  
 CC -1- SUBUNIT: Homotetramer. The tetramer is composed of two dimers. The  
 two subunits in a dimer are linked by a disulfide bond.  
 CC -1- TISSUE SPECIFICITY: Present in most cells except erythrocytes.  
 CC -1- MISCELLANEOUS: Cholinesterase is highly reactive with  
 organophosphate esters.  
 CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL, M99497; AAA37328.1; -  
 DR PIR, S70849; S70849.  
 DR HSSP, P22303; 1P8U.  
 DR MGD, MGI:894278; Behe.  
 DR InterPro, IPR002018; CarboxylesteraseB.

DR InterPro, IPR000997; Cholinesterase.  
 DR InterPro, IPR000379; Ser esters.  
 DR Pfam, PF00135; CHOLINESTRASE.  
 DR PRINTS, PR00878; CHOLINESTRASE.  
 DR PROSITE, PS00122; CARBOXYLESTERASE\_B\_1; 1.  
 DR PROSITE, PS00941; CARBOXYLESTERASE\_B\_2; 1.  
 KW Glycoprotein; Hydrolase; Serine esterase; Signal.  
 FT SIGNAL 1 29  
 FT CHAIN 30 603  
 FT ACT\_SITE 227 227 Cholinesterase.  
 FT ACT\_SITE 354 354 Acyl-ester intermediate (By similarity).  
 FT ACT\_SITE 467 467 Charge relay system (By similarity).  
 FT DISULFID 94 121 Charge relay system (By similarity).  
 FT DISULFID 281 292 By similarity.  
 FT DISULFID 429 548 By similarity.  
 FT DISULFID 600 600 Interchain (By similarity).  
 FT CARBOHYD 86 86 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 135 135 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 270 270 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 370 370 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 484 484 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 510 510 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 515 515 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 129 129 R -> P (in Ref. 2).  
 FT CONFLICT 129 129  
 SQ SEQUENCE 603 AA; 68521 MW; 719B1B2D0D1B5367 CnC64;

Query Match 81.1%; Score 2521; DB 1; Length 603;  
 Best Local Similarity 80.5%; Pred. No. 4,6e-181;  
 Matches 462; Conservative 47; Mismatches 65; Indels 0; Gaps 0;

QY 1 EDDIIATKNGKVRGMNLTVEGTTATFLGIPYAPPGRLRPFKPSGLTKMSDIWNTKX 60  
 DB 30 EEDFIITTKTGVRGIGSMPEVLGIVTAFLGIPYAPPGRLRPFKPSGLTKMSDIWNTKX 89  
 QY 61 YANSCQNDIOSEPPGSGSEMNPTDLSDELCLYANWIIPAKPKNATVLIWYGGGFOT 120  
 DB 90 YANSCYQNDIOAPPGFQSGSEMNPTDLSDELCLYANWIIPAKPKNATVLIWYGGGFOT 149  
 QY 121 GTSSLHVDKFLARVERIVYVSNRYGALGFLALPGNPEAPNGKLPDQGLAQWQK 180  
 DB 150 GTSSLHVDKFLARVERIVYVSNRYGALGFLALPGNPEAPNGKLPDQGLAQWQK 209  
 QY 181 NIAPGNGKSTLTPESAGASVSLHILSPGSHSLFTRALIQSGSFNAPNATVLYEAR 240  
 DB 210 NIAPGNGKSTLTPESAGASVSLHILSPGSHSLFTRALIQSGSFNAPNATVLYEAR 269  
 QY 241 NRTLNLAKLTGCSRENTEIILKLRKNDPOEILNLEAFVVPYGTPLSVNFGFTVDGDFLT 300  
 DB 270 NRTLNLAKLTGCSRENTEIILKLRKNDPOEILNLEAFVVPYGTPLSVNFGFTVDGDFLT 329  
 QY 301 DMEDILLEGQFKCTOILVGNKDBGTWLVYGAPEPSKDNLSLIRKKEFGSLNNYFPG 360  
 DB 330 DMHTLLQGLKVKKAQILVGVNDGEGAFVYGAPEPSKDNLSLIRKKEFGSLNNYFPG 389  
 QY 361 VSEFGESEILFHTDWDDORPENYREALGDVVDNFCIPALEFTKSEWGNNAFFY 420  
 DB 390 VSLRGEAVLFYVDWGEQSPVYDADVDVGDNIICPALEFTKRAELENNAFFY 449  
 QY 421 FEHRSSKLPWPEWGVHGYEIEFVGLPLERRDNTYKAEILSRIVKMANFAKYGNP 480  
 DB 450 FEHRSSKLPWPEWGVHGYEIEFVGLPLERRDNTYKAEILSRIVKMANFAKYGNP 509  
 QY 481 NETONNSTSPVPEKSTOKTLTNTSTRIMTLRAQOGRFMTSPFKYLEMNGINDAE 540  
 DB 510 NGTQGNSTWMPVFTSTOKTLTNTSTRIMTLRAQOGRFMTSPFKYLEMNGINDAE 569  
 QY 541 WEMKAGFHRNNYMMDMKQNFNDYTSKESCVGL 574  
 DB 570 QEMKAGFHRNNYMMDMKQNFNDYTSKESCVGL 603

RESULT 9

Q9JXCI





Db 390 SKAIESITFYTDWENQEKREHYRDAMDVIQDHYHICPAVEFAKTIAEVGNVFFYF 449

QY 422 EHRSSKLPMEPMGVHGVYIEFVGLPLERRDNYTKAEIILSRISVYKRNPAKYGNN 461

Db 450 EHRSSKLPMEPMGVHGVYIEFVGLPLERRDNYTKAEIILSRISVYKRNPAKYGNN 509

QY 482 ETONNSTSWVPVSTOCKYTLTNTESRIMTKRAOOCRWTSFPFVLEMTGNIDEAEW 541

Db 510 GTLLNGRMVFPSTOCKYTLTNTESRIMTKRAOOCRWTSFPFVLEMTGNIDEAEW 569

QY 542 EMKAGFHRNNYMMDMKQFNDYTSKKESCVG 573

Db 570 EMKAGFHRNNYMMDMKQFNDYTSKKESCVG 601

RESULT 11

ACES BRARE STANDARD; PRT; 634 AA.

AC 09DDE3;

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 01-OCT-2004 (Rel. 45, Last annotation update)

DB Acetylcholinesterase precursor (BC 3.1.1.7) (AChE).

OS Name=Ache;

GN Brachydanio rerio (Zebrafish) (Danio rerio).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;

OC Cyprinidae; Danio.

OX NCBI\_TaxID=7955;

RN 11

RP SEQUENCE FROM N.A.

RX MEDLINE=20576389; PubMed=11016933; DOI=10.1074/jbc.M06308200;

RA Bertrand C., Chatonnet A., Takke C., Yan Y., Postlethwait J.,

RA Toulant J.-P., Cousin X.;

RT "Zebrafish acetylcholinesterase is encoded by a single gene localized on linkage group 7. gene structure and polymorphism; molecular forms and expression pattern during development";

RT J. Biol. Chem. 276:464-474(2001).

RL

CC -1- FUNCTION: Rapidly hydrolyzes choline released into the synapse.

CC -1- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.

CC -1- SUBUNIT: Dimers and collagen-tailed forms, in which catalytic tetramers are associated with anchoring proteins that attach them to the basal lamina or to cell membranes. In the collagen-tailed forms, subunits are associated with a specific collagen, COLQ, which triggers the formation of isoform T tetramers from dimers.

CC -1- MISCELLANEOUS: No other isoforms exist. This protein corresponds to the T isoform in other species.

CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.

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CC -----

CC EMBL; AJ251640; CAC19790.1; -

DR HSSP; P04058; 1H23.

DR ZFIN; ZDB-GENE-010906-1; ache.

DR InterPro; IPR002018; CarboxylesteraseB.

DR InterPro; IPR000997; Cholinesterase.

DR InterPro; IPR000379; Ser esters.

DR Pfam; PF00135; Coesterase; 1.

DR PRINTS; PR00878; CHOLINESTRASE.

DR PROSITE; PS00122; CARBOXYLESTERASE\_B\_1; 1.

DR PROSITE; PS00941; CARBOXYLESTERASE\_B\_2; 1.

DR Glycoprotein; Hydrolase; Membrane; Neurotransmitter degradation;

KW Serine esterase; Signal; Synapse.

KW SIGNA 1 23 Potential.

FT CHAIN 24 634 Acetylcholinesterase.

FT ACT\_SITE 225 352 Acyl-ester intermediate (By similarity).

FT ACT\_SITE 352 352 Charge relay system (By similarity).

FT ACT SITE 495 495 Charge relay system (By similarity).

FT DISULFID 91 118 By similarity.

FT DISULFID 279 290 By similarity.

FT DISULFID 427 580 By similarity.

FT DISULFID 631 651 Interchain (By similarity).

FT CARBOHYD 133 133 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 184 184 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 283 283 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 368 368 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 512 512 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 592 592 N-linked (GlcNAc...) (Potential).

SQ SEQUENCE 634 AA; 71998 MW; 47F348BA87C1E52 CRC64;

Query Match 56.8%; Score 1765.5; DB 1; Length 634;

Best local similarity 53.0%; Pred. No. 3.9e-124;

Matches 323; Conservative 106; Mismatches 144; Indels 37; Gaps 6;

QY 1 EDDIIATKNGKVRGMNLTVFGGT-VTAFGLGFPYAGPLGRIRPKKPSQSLTWSIDIMNT 59

Db 26 EPDLVAVATRLAGVOGTRLPVDPDRSHVIAFLGIPYAEPPIGKRRFRAEKKEKMNWPEAK 85

QY 60 KYANSCCONIDOSPFGHSEMMNPVTLSEDCIYLNWVI-DAPRKATVLIWYGGGF 118

Db 86 EFSNACTQGVDTSYRPFPGFPIEMNPRKWSIEDCIYLNWVPTPRQNLTVWVWYIGGFF 145

QY 119 QTGTSSLHYDGGKFLARVERVTVSMNRYVGLAFLPAGNDEAPGNMGLFPQQLALQWV 178

Db 146 YSGSSSLDYVDGRYLAYTEKVVVSVNRYVGAFGFIALNGSSDADAGNVGLYDORLALQWV 205

QY 179 QKXIAAFGNGPKSVTLFGSSAGAAVSLLSLPGSHSLFTRAILLOGSPNAPMAVTSLE 238

Db 206 QENIHFFGNGPKVITFGSSAGAAVSVMVLSBDSPLFTRAILLOGSPNAPMAVTSLE 265

QY 239 ARNRNTLAKLTCGSRNETETIIKCLRNDPOEILINAEFVVPYGTPLSVNGFPTVDPF 298

Db 266 ARNRITLGLKLVCTGNDTELICLRNHPELIDQENQVLPWSSLFFPSFVPTVDGVF 325

QY 299 LITMDPILLETGQFKTQILVGNKDEGTFLVYGAPGFSKONNSITTRKEPQGLKTF 358

Db 326 FPDTPAMTSSGFKTQILLVGNQDEGSYFLIYGAPGFSKONNSITTRKEPQGLKTF 385

QY 359 PGVSEKGEIILHYTDWDDQRPENYRRLGVGDVNYPCALFEFTKFSF----- 411

Db 386 PHANDIGLEAVLIQYTDMDENNQGRNDMDVIDQVNTICLQHPAKSYAOYALAHQ 445

QY 412 -----WGNN-----AFYYPERHSSKLPMEPMGVHGVYIEFVGL 448

Db 446 SSAARPTLGWNSGPTGVNNSGSHGAVIYLPDRHASNLAWEPMGVHGVYIEFVGL 505

QY 449 PLERDNYTKAEIILSRISVYKRNPAKYGNN-----ETONNSTSWVPVSTOCKYTLTN 504

Db 506 PLEKRLVYTAEEKLSRIRIRYANFARTGNPVNTDGTDSRRRWPQFSANQKVGGLN 565

QY 505 TETRIRITKRAOOCRWTSFPFVLEMTGNIDEAEWEMVGHRRNNYMMDMKQFNDY 564

Db 566 TEPKWKVGLRTQFCALMNFPLRLNITNTIDVERQKVEHRHSSYMMHMKSGQFDH 625

QY 565 TSKKESCVGL 574

Db 626 -SKQERCTDL 634

RESULT 12

ACES EMBL STANDARD; PRT; 633 AA.

AC 042275;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 01-OCT-2004 (Rel. 45, Last annotation update)

DB Acetylcholinesterase precursor (BC 3.1.1.7) (AChE).

OS Electrophorus electricus (Electric eel).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Gymnotiformes;



CC Electrophoridae; Electrophorus.  
 OX NCBI\_Taxid=8005;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98070504; PubMed=9407087;  
 RA Simon S., Massoulié J.;  
 RT "Cloning and expression of acetylcholinesterase from Electrophorus.  
 RT Splicing pattern of the 3' exons in vivo and in transfected mammalian  
 RT cells.";  
 RL J. Biol. Chem. 272:33045-33055 (1997).  
 CC -1- FUNCTION: Rapidly hydrolyzes choline released into the synapse.  
 CC -1- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.  
 CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.  
 CC -----  
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 CC -----  
 DR EMBL, AF030422; AAB86606.1; -  
 DR HSP, P04058; I123.  
 DR InterPro: IPR002018; CarbesteraseB.  
 DR InterPro: IPR000997; Cholinesterase.  
 DR InterPro: IPR000379; Ser estse.  
 DR Pfam: PF00135; Coesterase; 1.  
 DR PRINTS: PRO0878; CARBOXYL-ESTERASE.  
 DR PROSITE: PS00122; CARBOXYL-ESTERASE\_B\_1; 1.  
 DR PROSITE: PS00941; CARBOXYL-ESTERASE\_B\_2; 1.  
 KM Glycoprotein; Hydrolyase; Membrane; Neurotransmitter degradation;  
 KM Serine esterase; Signal; Synapse.  
 FT SIGNAL 1 23 Potential.  
 FT CHAIN 24 633 Acetylcholinesterase.  
 FT ACT\_SITE 225 225 Acyl-ester intermediate (By similarity).  
 FT ACT\_SITE 352 352 Charge relay system (By similarity).  
 FT ACT\_SITE 494 494 Charge relay system (By similarity).  
 FT DISULFID 91 118 By similarity.  
 FT DISULFID 279 290 By similarity.  
 FT DISULFID 427 579 By similarity.  
 FT DISULFID 630 630 Interchain (By similarity).  
 FT CARBOHYD 133 133 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 184 184 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 283 283 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 368 368 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 511 511 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 591 591 N-linked (GlcNAc...) (Potential).  
 SQ SEQUENCE 633 AA; 71814 MW; FC92FE7E4ADB84C3 CRC64;  
 Query Match 56.8%; Score 1765; DB 1; Length 633;  
 Best Local Similarity 53.2%; Pred. No. 4.3e-124; Indels 36; Gaps 6;  
 Matches 324; Conservative 103; Mismatches 146;  
 QY 1 EDIIATKNGKVKGMNLYFGGT-VTAFLGIPIYAOPPLGLRFRKQSLTKMSDINWAT 59  
 DB 26 DPELTITMRLGQVGTPLPVDNRSHVIAFLGIPFAEPPLGMRKRPKPPKMDVDGAR 85  
 QY 60 KYANSCQNDIQSPGPHGSEMMNPNTDLSBDCIYLVNWPFA-RPKKATYLTITYGGEF 118  
 DB 86 DYPACQYQYVDTSPGSGTEMMNPNRMMSBDCIYLVNWPATRPFHLTYMVIYGGGF 145  
 QY 119 QYTGSSLVHVDGKRLAVERYIVSMYRVAGLFLALPGRPBAPGMNGGLDQDLALQWV 178  
 DB 146 YSGSSSLDVVDGKRLAVSEKVVSMYRVSAFGLFLANGSABAPGVGLDQDLALQWV 205  
 QY 179 QKNIAAGPKPKSVTLFGESAGAAVSLSLSPSHSLFTRAILQSGSFNAPMAVTSIYE 238  
 DB 206 QDNTHFGGNPKQYTLFGESAGAAVSGLHSLSPSRPFTALIQSGVNGPMKTVSPDE 265  
 QY 239 ARNTALAKLTGCSRENETIYKLRKNDQQLLEAFVPPVPTPLSVNFGTVGDGF 298  
 DB 266 ARRAIKRLGVCPDNDITDLIDCLRSKOPDIDQEMVLPSGGLFRFSFVVIDGV 325

QY 299 LTDPDILLELQGFKKTQIIVGVNKGEGTWFLVYGAFFSKDNNSITTRKEFOGLKIF 358  
 DB 326 PPDTPAMLNSGNPKDQIILGVNNGESYFLIYGAFSGKDNLSLITREDPLQGVKMSV 385  
 QY 359 PGVSEFGKESILFRYTTWVDQRPENRREALGVNGVYNTICPALETKKFSB----- 411  
 DB 386 PHANEIGLEAVIILQYTTDMEDNDPIKREAMDIDVGHNVVCPLOHFAKMYAQSIILQOQ 445  
 QY 412 -----MGN-----NAFYFPHRSKSLPMPWMGVHGEIEFVGLP 449  
 DB 446 TGRASQNLGKNGSGASNGNSQVSYLYMFDHRASNLVWPEMGIHGEIEFVGLP 505  
 QY 450 LERRDNTKAEILSRISIVKMANFAYKGNPNETONNSTS-----WPVFKSTQKYLTLNT 505  
 DB 506 LERKINTLEBEKLSRMMKMYMANFATGNPNINVDGISRRRWPFVSTEQHVGILNT 565  
 QY 506 ESTRIKTKRAQOCRFSTFPFKYLENTGIDAEWMAKGFHRMNNYMDKMQFNDYT 565  
 DB 566 DSLKVKHGLKSQFCALWNRPLPRLVNTENIDDAERQWKAEPFRMSYMMHWKXQFDHY- 624  
 QY 566 SKKSCVGL 574  
 DB 625 SKDERTNL 633  
 RESULT 13  
 ACES\_BUNFA STANDARD; PRT; 606 AA.  
 ID ACES\_BUNFA STANDARD; PRT; 606 AA.  
 AC Q92035; O73748; Q10720;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 10-OCT-2003 (Rel. 42, Last sequence update)  
 DT 01-OCT-2004 (Rel. 45, Last annotation update)  
 DE Acetylcholinesterase precursor (EC 3.1.1.7) (AChE).  
 OS Bungarus fasciatus (Banded krait).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Elapidae; Bungarinae; Bungarus.  
 OX NCBI\_Taxid=6613;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM S).  
 RC TISSUE=Venom gland;  
 RX MEDLINE=96279007; PubMed=8662867;  
 RA Cousin X., Bon S., Duval N., Massoulié J., Bon C.;  
 RT "Cloning and expression of acetylcholinesterase from Bungarus  
 RT fasciatus venom. A new type of COOH-terminal domain; involvement of a  
 RT positively charged residue in the peripheral site.";  
 RL J. Biol. Chem. 271:15099-15108 (1996).  
 RN [2]  
 RP SEQUENCE OF 512-606 FROM N.A. (ISOFORMS S AND T), SUBUNIT, AND TISSUE  
 RP SPECIFICITY.  
 RC TISSUE=Liver, and Muscle;  
 RX MEDLINE=98212017; PubMed=9545320;  
 RA Cousin X., Bon S., Massoulié J., Bon C.;  
 RT "Identification of a novel type of alternatively spliced exon from the  
 RT acetylcholinesterase gene of Bungarus fasciatus. Molecular forms of  
 RT acetylcholinesterase in the snake liver and muscle.";  
 RL J. Biol. Chem. 273:9812-9820 (1998).  
 RN [3]  
 RP SEQUENCE OF 206-220; 253-272; 321-340; 347-372 AND 503-511.  
 RC TISSUE=Venom;  
 RX MEDLINE=96244524; PubMed=8674549;  
 RA Cousin X., Cremonon C., Graesi J., Meflah K., Cornu G., Sallou B.,  
 RA Bon S., Massoulié J., Bon C.;  
 RT "Acetylcholinesterase from Bungarus venom: a monomeric species.";  
 RL FEBS Lett. 387:196-200 (1996).  
 CC -1- FUNCTION: Rapidly hydrolyzes choline released into the synapse.  
 CC -1- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.  
 CC -1- SUBUNIT: Isoform S is monomeric. Isoform T can form oligomers,  
 CC including collagen-tailed forms.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;



RA Chhajlala V., Derr D., Earles B., Schmell E., August T. ;  
RT "Purification and partial amino acid sequence analysis of human  
RL erythrocyte acetylcholinesterase." ;  
RN FEBS Lett. 247:279-282(1989).  
RN [5]  
RP MUTAGENESIS OF CYS-611.  
RX MEDLINE=92084699; PubMed=1748670;  
RA Velan B., Grosfeld H., Kromman C., Leitner M., Gozes Y., Lazar A.,  
RT Flashner Y., Marcus D., Cohen S., Shafferman A. ;  
RA "The effect of elimination of intersubunit disulfide bonds on the  
RT activity, assembly, and secretion of recombinant human  
RT acetylcholinesterase. Expression of acetylcholinesterase Cys-580-->Ala  
RT mutant." ;  
RL J. Biol. Chem. 266:23977-23984(1991).  
RN [6]  
RP MUTAGENESIS OF ACTIVE SITE RESIDUES AND OF ASP-206 AND ASP-435.  
RX MEDLINE=92388112; PubMed=1517212;  
RA Shafferman A., Kromman C., Flashner Y., Leitner M., Grosfeld H.,  
RT Orendelich A., Gozes Y., Cohen S., Ariel N., Barak D. ;  
RA "Mutagenesis of human acetylcholinesterase. Identification of residues  
RT involved in catalytic activity and in polypeptide folding." ;  
RL J. Biol. Chem. 267:17640-17648(1992).  
RN [7]  
RP 3D-STRUCTURE MODELING OF 35-574.  
RX MEDLINE=98304745; PubMed=9640563;  
RA Felder C.E., Botli S.A., Lifson S., Silman I., Sussman J.L. ;  
RT "External and internal electrostatic potentials of cholinesterase  
RT models." ;  
RL J. Mol. Graph. Model. 15:318-327(1997).  
RN [8]  
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 36-574.  
RX MEDLINE=20508217; PubMed=11053835; DOI=10.1107/S0907444900010659;  
RA Kryger G., Barak M., Gilek K., Tokar L., Velan B., Lazar A.,  
RT Kromman C., Barak D., Ariel N., Shafferman A., Silman I.,  
RA Sussman J.L. ;  
RT "Structures of recombinant native and E202Q mutant human  
RT acetylcholinesterase complexed with the snake-venom toxin fasciculin-  
RT 11." ;  
RL Acta Crystallogr. D 56:1385-1394(2000).  
RN [9]  
RP VARIANT BLOOD GROUP YT(B) ASN-353.  
RX MEDLINE=93256075; PubMed=8488842;  
RA Bartels C.F., Zelinski T., Lockridge O. ;  
RT "Mutation at codon 322 in the human acetylcholinesterase (ACHE) gene  
RT accounts for YT blood group polymorphism." ;  
RL Am. J. Hum. Genet. 52:928-936(1993).  
CC -1- FUNCTION: Rapidly hydrolyzes choline released into the synapse.  
CC -1- CATALYTIC ACTIVITY: Acetylcholine + H(2O) = choline + acetate.  
CC -1- SUBUNIT: Homotetramer; composed of disulfide-linked homodimers.  
CC -1- INTERACTIONS: Interacts with PRIMA1. The interaction with PRIMA1 is required to  
CC anchor it to the basal lamina of cells and organize into tetramers  
CC (by similarity).  
CC -1- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Comment=Additional isoforms seem to exist;  
CC Name=1;  
CC IsoId=P22303-1; Sequence=Displayed;  
CC Name=2;  
CC IsoId=P22303-2; Sequence=VSP\_001457;  
CC -1- POLYMORPHISM: AChE is responsible for the Yt blood group system.  
CC The molecular basis of the Yt(a)=Yt1/Yt(b)=Yt2 blood group  
CC antigens is a single variation in position 353; His-353  
CC corresponds to Yt(a) and the rare variant with Asn-353 to Yt(b).  
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.  
CC -1- DATABASE: NMBE=Blood group antigen mutation database;  
CC NOTE=Yt blood group system;  
CC WWW="http://www.bloc.secom.yu.edu/bgmut/Yt.htm".  
CC -----  
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CC	-----			
DR	EMBL; M55040; AAA68151.1; .			
DR	EMBL; AF5312032; AAK21003.1; .			
DR	EMBL; S71129; AAC60618.1; .			
DR	PIR; A39256; A39256.			
DR	PDB; 1B41; X-ray; A=36-574.			
DR	PDB; 1F8U; X-ray; A=32-614.			
DR	PDB; 2CLJ; Model; @=32-574.			
DR	SWISS-2DPAGE; P22303; HUMAN.			
DR	GeneW; HGNC:108; ACHB.			
DR	MIM; 112100; .			
DR	MIM; 112100; .			
DR	GO; GO:0005605; C:basal lamina; NAS.			
DR	GO; GO:0005576; C:extracellular; NAS.			
DR	GO; GO:0042166; F:acetylcholine binding; NAS.			
DR	GO; GO:0003990; F:acetylcholinesterase activity; IMP.			
DR	GO; GO:0001540; F:beta-amyloid binding; NAS.			
DR	GO; GO:0042803; F:protein homodimerizing activity; NAS.			
DR	GO; GO:0001507; F:p-amyloid precursor protein breakdown in synaptic clef; NAS.			
DR	GO; GO:0007155; P:amyloid precursor protein metabolism; NAS.			
DR	GO; GO:0007155; P:cell adhesion; NAS.			
DR	GO; GO:0008283; P:cell proliferation; NAS.			
DR	GO; GO:0006260; P:DNA replication; NAS.			
DR	GO; GO:0007174; P:muscle development; NAS.			
DR	GO; GO:00050714; P:positive regulation of protein secretion; NAS.			
DR	GO; GO:0009611; P:response to wounding; NAS.			
DR	GO; GO:0007416; P:synaptogenesis; NAS.			
DR	InterPro; IPR002018; Carboxesterase.			
DR	InterPro; IPR000997; Cholinesterase.			
DR	InterPro; IPR000379; Ser_ester.			
DR	Pfam; PF00135; Coesterase; 1.			
DR	PRINTS; PR00878; CHOLINESTRASE.			
DR	PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.			
DR	PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.			
KM	3d-structure; Alternative splicing; Blood group antigen;			
KM	Direct protein sequencing; Glycoprotein; Hydrolase; Membrane;			
KM	Neurotransmitter degradation; Polymorphism; Serine esterase; Signal;			
KM	Synapse.			
FT	SIGNAL	1	31	Potential.
FT	CHAIN	32	614	Acetylcholinesterase.
FT	ACT SITE	234	234	Acyl-ester intermediate.
FT	ACT SITE	365	365	Charge relay system.
FT	ACT SITE	478	478	Charge relay system.
FT	DISULFID	100	127	
FT	DISULFID	288	303	
FT	DISULFID	440	560	Interchain.
FT	DISULFID	611	611	N-linked (G1CNAC. . .) (Potential).
FT	CARBOHYD	296	296	N-linked (G1CNAC. . .) (Potential).
FT	CARBOHYD	381	381	N-linked (G1CNAC. . .) (Potential).
FT	CARBOHYD	495	495	DTIDEARQKRAKRPKSSVYMKKQPDHYSKDRCSDL
FT	VASPLIC	575	614	-> GMSQPSAGRGYGAQCNPSLPLASBASTPGRFT
FT				HGEAAPPGLPLLLHLLFLSHLRL (in
FT				isoform 2).
FT				/FtId=VSP_001457.
FT				V -> E (in dbSNP:8286).
FT	VARIANT	333	333	/FtId=VAR_011934.
FT	VARIANT	353	353	H -> N (in YcDb) antigen; dbSNP:1799605).
FT	MUTAGEN	206	206	/FtId=VAR_002359.
FT	MUTAGEN	234	234	D->N: Misfolding; absence of secretion.
FT	MUTAGEN	365	365	E->A: Loss of activity.
FT	MUTAGEN	435	435	D->N: Misfolding; absence of secretion.
FT	MUTAGEN	478	478	H->A: Loss of activity.
FT	MUTAGEN	611	611	C->A: Impairment of Interchain disulfide
FT	TURN	38	39	bridge formation.
FT	STRAND	40	42	
FT	STRAND	47	49	
FT	STRAND	51	53	
FT	TURN	56	57	





GN Name-Ache;  
 OS Mus musculus (mouse).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 CC NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=90380429; PubMed=2400605;  
 RX Rachinsky T.L., Camp S., Li Y., Ekstrom T.J., Newton M., Taylor P.;  
 RT "Molecular cloning of mouse acetylcholinesterase: tissue distribution  
 of alternatively spliced mRNA species.";  
 RL Neuron 5:317-327(1990).  
 RP [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/SV;  
 RX MEDLINE=2118439; PubMed=11239002;  
 RA Wilson M.D., Riemer C., Martinale D.W., Schnupf P., Boright A.P.,  
 RA Cheung T.L., Hardy D.W., Schwartz S., Scherer S.W., Tsai L.-C.,  
 RA Miller W., Koop B.P.;  
 RT "Comparative analysis of the gene-dense AChE/TFR2 region on human  
 chromosome 7q22 with the orthologous region on mouse chromosome 5.";  
 RL Nucleic Acids Res. 29:1352-1365(2001).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Retina;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Krausberg R.L., Feingold E.A., Grouse L.H., Derge U.G.,  
 RA Strausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Canninci P., Krangel C.,  
 RA Rana S.S., Loughellano N.A., Peters G.J., Abramson R.D., Mulhaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.U., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.C., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A.C., Rodriguez S., Sanchez A.,  
 RA Whiting J., Madan A., Young A.C., Shvachenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [4]  
 RP INTERACTION WITH PRIMA1.  
 RX MEDLINE=21664287; PubMed=11804574;  
 RA Perrier A.L., Maesoulie J., Krejci E.;  
 RT "PRIMA1, the membrane anchor of acetylcholinesterase in the brain.";  
 RL Neuron 33:275-285(2002).  
 RN [5]  
 RP X-RAY CRYSTALLOGRAPHY (3.2 ANGSTROMS) OF COMPLEX WITH FASCICULIN.  
 RX MEDLINE=9607648; PubMed=8521480;  
 RA Bourne Y., Taylor P., Marchot P.;  
 RT "Acetylcholinesterase inhibition by fasciculin: crystal structure of  
 the complex.";  
 RL Cell 83:503-512(1995).  
 RN [6]  
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).  
 RX MEDLINE=99115643; PubMed=9915834;  
 RA Bourne Y., Taylor P., Bougis P.E., Marchot P.;  
 RT "Crystal structure of mouse acetylcholinesterase. A peripheral site-  
 occluding loop in a tetrameric assembly.";  
 RL J. Biol. Chem. 274:2963-2970(1999).  
 RN [7]  
 RP X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF 34-573 IN COMPLEX WITH  
 RP INHIBITOR.  
 RX PubMed=12505979; DOI=10.1093/emboj/cdg005;  
 RA Bourne Y., Taylor P., Radic Z., Marchot P.;  
 RT "Structural insights into ligand interactions at the  
 acetylcholinesterase peripheral anionic site.";

RL EMBL J. 22:1-12(2003).  
 CC -1- FUNCTION: Rapidly hydrolyzes choline released into the synapse.  
 CC -1- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.  
 CC -1- SUBUNIT: Isoform H generates GPI-anchored dimers, disulfide  
 CC linked. Isoform T generates multiple structures, ranging from  
 CC monomers and dimers to collagen-tailed and hydrophobic-tailed  
 CC forms, in which catalytic tetramers are associated with anchoring  
 CC proteins that attach them to the basal lamina or to cell  
 CC membranes. In the collagen-tailed forms, isoform T subunits are  
 CC associated with a specific collagen, COG, which triggers the  
 CC formation of isoform T tetramers, from monomers and dimers (by  
 CC similarity). Interacts with PRIMA1. The interaction with PRIMA1 is  
 CC required to anchor it to the basal lamina of cells and organize  
 CC into tetramers.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=T;  
 CC IsoId=P21836-1; Sequence=Displayed;  
 CC Name=H;  
 CC IsoId=P21836-2; Sequence=Not described.  
 CC Note=No experimental confirmation available;  
 CC -1- TISSUE SPECIFICITY: Predominates in most expressing tissues except  
 CC erythrocytes where a glycopospholipid-attached form of AChE  
 CC predominates.  
 CC -1- MISCELLANEOUS: Synapses usually contain asymmetric molecules of  
 CC cholinesterase, with a collagen-like part disulfide-bonded to the  
 CC catalytic part. A different, globular type of cholinesterase  
 CC occurs on the outer surfaces of cell membranes, including those of  
 CC erythrocytes. This is the catalytic subunit of an asymmetric or  
 CC soluble form of AChE.  
 CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.  
 CC -----  
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 CC -----  
 CC EMBL: X65518; CA39867.1; -;  
 CC EMBL: AF312033; AA28816.1; -;  
 CC EMBL: BC046327; AA46327.1; -;  
 CC PIR: JH0314; JH0314.  
 CC PDB: 1C2B; X-ray; A/B=35-573.  
 CC PDB: 1C2D; X-ray; A/B/C/D=36-574.  
 CC PDB: 1U06; X-ray; A/B=32-574.  
 CC PDB: 1U07; X-ray; A/B=32-574.  
 CC PDB: 1K06; X-ray; A=32-580.  
 CC PDB: 1MAA; X-ray; A/B/C/D=32-578.  
 CC PDB: 1MAH; X-ray; A=32-574.  
 CC PDB: 1NSW; X-ray; A/B=32-572.  
 CC PDB: 1NSR; X-ray; A/B=32-574.  
 CC PDB: 1Q83; X-ray; A/B=1-580.  
 CC MGD: MGI:87876; Ache.  
 CC GO: GO:0045202; C:synapse; IDA.  
 CC InterPro: IPR002018; Carboxylesterase.  
 CC InterPro: IPR000997; Cholinesterase.  
 CC InterPro: IPR000379; Ser\_estr.  
 CC Pfam: PF00135; Coesterase; 1.  
 CC PRINTS: PR00878; CHOLINESTERASE.  
 CC PROSITE: PS00122; CARBOXYLESTERASE B 1, 1.  
 CC PROSITE: PS00941; CARBOXYLESTERASE B 2, 1.  
 CC 3D-structure: Alternative splicing; Glycoprotein; Hydroxylase; Membrane;  
 CC Neurotransmitter degradation; Serine esterase; Signal; Synapse.  
 CC SIGNAL  
 CC CHAIN 1 31  
 CC ACT\_SITE 32 614 Acetylcholinesterase.  
 CC ACT\_SITE 234 Acyl-ester intermediate.  
 CC ACT\_SITE 365 365 Charge relay system.  
 CC ACT\_SITE 478 478 Charge relay system.  
 CC DISULFID 100 127  
 CC DISULFID 288 303

FT DISULFID 440 560  
 FT DISULFID 611 611 Interchain (By similarity).  
 FT CARBOHYD 296 296 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 381 381 N-linked (GlcNAc...)  
 FT CARBOHYD 495 495 N-linked (GlcNAc...)  
 FT HELIX 37 39  
 FT STRAND 40 43  
 FT TURN 44 45  
 FT STRAND 46 49  
 FT STRAND 51 55  
 FT TURN 56 57  
 FT STRAND 58 67  
 FT STRAND 69 69  
 FT HELIX 74 76  
 FT TURN 77 78  
 FT STRAND 83 83  
 FT STRAND 90 92  
 FT STRAND 94 94  
 FT STRAND 99 100  
 FT TURN 109 110  
 FT HELIX 112 115  
 FT TURN 116 117  
 FT STRAND 123 124  
 FT STRAND 129 135  
 FT STRAND 143 149  
 FT TURN 153 155  
 FT TURN 159 160  
 FT HELIX 162 164  
 FT HELIX 167 173  
 FT STRAND 176 180  
 FT HELIX 185 189  
 FT TURN 193 194  
 FT HELIX 202 217  
 FT HELIX 218 221  
 FT TURN 222 222  
 FT STRAND 223 233  
 FT TURN 234 234  
 FT HELIX 235 244  
 FT TURN 245 245  
 FT HELIX 247 250  
 FT STRAND 251 252  
 FT STRAND 255 259  
 FT STRAND 270 271  
 FT HELIX 272 285  
 FT TURN 286 287  
 FT HELIX 297 304  
 FT TURN 305 306  
 FT HELIX 309 315

Query Match 53.9%; Score 1675.5; DB 1; Length 614;  
 Best Local Similarity 52.8%; Pred. No. 2,3e-117;  
 Matches 306; Conservative 104; Mismatches 163; Indels 7; Gaps 4;

QY 1 EDDIIATKNGKVGKMLVFGGTATFLGIPIYAPPLGLRFPKPSQSLTKMSDIMNATK 60  
 DB 36 DPOLIVVRGQLRGIRLTKAPGVSAFLGIPFAPPGSRRFPMPKPKPWSGVLDATT 95  
 QY 61 YANSCCNINQSPFGHFGSEMMNNTDLSBCLYLNWIPAKPKKNT-VLWITYGGGFQ 119  
 DB 96 FQNVCGYVDTLPGFEGTEMMNRLSEDCLYLNWTPYPRASLPVLIWITYGGGFY 155  
 QY 120 TGTSLIVYDGKFLARVERVIVSMNRYGALGFALPGNPEAPGNKGLFPQDLALQMVQ 179  
 DB 156 SGAAASLDVYDGRFLAIVEGAVIVSMNRYVGFGLALPGSREAPGNVGLDQRLALQMVQ 215  
 QY 180 KNIAAFGNGKSVTLTFESAGASVSLHLSPGSHLFTPAITLQSSFPNPAWATSLYE 239  
 DB 216 ENIAAFGSDPMSVTLTFESAGASVGMHILSLPERSLFHRAVLOSCTPNCGFMAVTSAGEA 275  
 QY 240 RNTPLNLAKLTGC---SRENETEITKLNKDPQELLNEAFVVPYGTPLSVNFGPTVD 295  
 DB 276 RRRATLRLVGCPPGAGGNDTLLACLRTPRADLVDEHMYLFPQESIFRFSFVAVD 335

QY 296 GDFLTMDPDLLEIGQKKTQILVGNKKDGTWFLVYGAFGSKDNNSITRKEFORGLK 355  
 DB 336 GDFSLDPDLLEINTGDDQDQVLVGVVXKDGSGYFLVGVGFSKDNLSLSRAQFLAGVR 395  
 QY 356 IFPPGVSEPKESILFHYTMDVDQRENTREBALGDVGVGNFPCPLLEFTKKSEMGNN 415  
 DB 396 IGVFQASDILAFAVLLVYTMLEHEDPTHLRDNASAVGDNVVCPPAQLAGRLAAGAR 455  
 QY 416 AFYYFHEHRSKSLPWPMMGMGMHGYEIEFVFGHPLERDNYTKAEILSRIVRWANFA 475  
 DB 456 VYAVIFHRASLTLPWPMGVPHCYEIEFGLPLDPSLNTYTBERTFAQRLMKWYNFA 515  
 QY 476 KYGNPNETQNN-STSWPEKSTQKYLTLNTESTRTMTKLRQAQCRFTSPPKVLEMTG 534  
 DB 516 RTGDPNDPRDSKSPQWPPYTTAAQOYVSLMKPLEVVRGRLAQCAPWNRFLPYLLSATD 575  
 QY 535 NIDEAEWEMKAGFHRKNNVMMDKNPNQNDTSKESCVGL 574  
 DB 576 TLDEAERQWKAEPFRMSYVHWKNQPDHY-SKQERCSDL 614

## RESULT 18

ID BAC31228 PRELIMINARY; PRT; 614 AA.  
 AC BAC31228;  
 DT 14-APR-2004 (TREMBlrel. 27, Created)  
 DT 14-APR-2004 (TREMBlrel. 27, Last sequence update)  
 DT 14-APR-2004 (TREMBlrel. 27, Last annotation update)  
 DE 3 days neonate thymus cDNA, RIKEN full-length enriched library,  
 DE clone:A630083607 product:acetylcholinesterase, full insert  
 DE sequence.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Thymus;  
 RX MEDLINE=22354683; PubMed=12466851;  
 RA The FANTOM Consortium.  
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs.";  
 RL Nature 420:563-573 (2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Thymus;  
 RX MEDLINE=21085660; PubMed=11217851;  
 RA RIKEN FANTOM Consortium;  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690 (2001).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Thymus;  
 RX MEDLINE=9279253; PubMed=10349636;  
 RA Carninci P., Hayashizaki Y.,  
 RT "High-efficiency full-length cDNA cloning.";  
 RL Meth. Enzymol. 303:19-44 (1999).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Thymus;  
 RX MEDLINE=2049374; PubMed=11042159;  
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.,  
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";  
 RL Genome Res. 10:1617-1630 (2000).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Thymus;  
 RX MEDLINE=20530913; PubMed=11076861;  
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
 RA Kono H., Akiyama J., Nishi K., Katsunai T., Tashiro H., Itoh M.,



RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
 RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,  
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,  
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
 RA "RIKEN integrated sequence analysis (RISA) system-384-format  
 RT sequencing pipeline with 384 multicapillary sequencer";  
 RL Genome Res. 10:1757-1771(2000).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Thymus;  
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,  
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,  
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohnato N., Okazaki Y.,  
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,  
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,  
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AK042335; BAC31228.1; -  
 SQ SEQUENCE 614 AA; 68168 MW; 66E2512463C21172 CRC64;  
 Query Match 53.9%; Score 1675.5; DB 2; Length 614;  
 Best Local Similarity 52.8%; Pred. No. 2,3e-117; Indels 7; Gaps 4;  
 Matches 306; Conservative 104; Mismatches 163;  
 QY 1 EDDIIATKNGKVRGNMLTVFGTVAFLGIPIYAPPLGRLRFKKPSLTKMSDINATK 60  
 Db 36 DPGLVAVRGQGLKIRLKAPEGVSAFLGIPFAEPVGSRRFPPKPKWSGVLDAT 95  
 QY 61 YANSCCNIDGSPFGHSGEMWNTDLSBCLYLTNWIAPKPKKAT-VLTWYGGGFG 119  
 Db 96 FQNVCCYVDVLTLPFGFTEGMNRELSBCLYLTNWIAPKPKKAT-VLTWYGGGFG 155  
 QY 120 TGTSSLHYDGGKFLARVERVIVSMNRVGAFLGALPGNPEAPGNGLFDQDLATQMV 179  
 Db 156 SGASASLVYDRFLAQVGBAVLVSMNRYGVFGFLALPGSEAPGNGLDQDLATQMV 215  
 QY 180 KNIAFGNPKSVTLTFESAGASVSLHLLSPGSHSLFTRAILGSSGFNAPWATSLYE 239  
 Db 216 ENIAFGDPMSTVTLFGESAGASVGMHLLSLPERSLFHRAVLQSGTPNGFWATVSGEA 275  
 QY 240 NRRRLNLAQLTGC-----SRENETIICLRKRDQOEILLNARFVPGTPISTVAPGTV 295  
 Db 276 RRRATYLLARLVGCPGGAGGNDTELICLRKRPADQDLVDEHMHVLPQESIFRSFVVD 335  
 QY 296 GDFLTMDPDLLELGOFKTQILVGVNDEGTFWLVYGAPEFSKDNNSITRKEFOGLK 355  
 Db 336 GDFLSTDPDLALJNGDDPQDLVLVGVNDEGTFWLVYGAPEFSKDNNSITRKEFOGLK 395  
 QY 356 IFFPGVSEFGKESLFTYTDVNDQRPENYBALGDVGVNFCPLAEFKKSEWGN 415  
 Db 396 IGVQASDLAEAVLHTYTDVNDQRPENYBALGDVGVNFCPLAEFKKSEWGN 455  
 QY 416 AFYFYEHRSSKLPWPMWGMHGEIEFVFGPLERDNTYKAELISIRSVRMNFA 475  
 Db 456 VYATIFERRASTLTWPLMWSVPHGEIEFVFGPLERDNTYKAELISIRSVRMNFA 515  
 QY 476 KYGNPNETQNN-STSWPVFKSTQKYLTLNTESTRTIMTKLRAOQCFWTSFFPYLVETG 534  
 Db 516 RTGDPNDPRDSKSPQWPPYTTAAQOYVSLNKLPLEVRGRLAQTCAPNNRFLPILSLTD 575  
 QY 535 NIDEAEWEMKAGFHRMNNYMDKXQPNVDYTSKESCTGL 574  
 Db 576 TLDEAEQWKABEFHRMSSYVMWKQDFHY-SKQRCSDL 614

ID BAC31641 PRELIMINARY; PRT; 614 AA.  
 AC BAC31641;  
 DT 14-APR-2004 (TREMBLrel. 27, Created)  
 DT 14-APR-2004 (TREMBLrel. 27, Last sequence update)  
 DT 14-APR-2004 (TREMBLrel. 27, Last annotation update)  
 DE 10 days neonate cortex cDNA, RIKEN full-length enriched library,  
 DE clone: A830027P05 product: acetylcholinesterase, full insert  
 DE sequence.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Cortex;  
 RA MEDLINE=22354683; PubMed=12466851;  
 RA The FANTOM Consortium.  
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs";  
 RL Nature 420:563-573 (2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Cortex;  
 RX MEDLINE=21085660; PubMed=11217851;  
 RA RIKEN FANTOM Consortium;  
 RT "Functional annotation of a full-length mouse cDNA collection";  
 RL Nature 409:685-690 (2001).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Cortex;  
 RX MEDLINE=99279253; PubMed=10349636;  
 RA Carninci P., Hayashizaki Y.;  
 RT "High-efficiency full-length cDNA cloning";  
 RL Meth. Enzymol. 303:19-44 (1999).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Cortex;  
 RX MEDLINE=20499374; PubMed=11042159;  
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
 RT "Normalization and subcloning of cap-trapper-selected cDNAs to  
 RT prepare full-length cDNA libraries for rapid discovery of new genes";  
 RL Genome Res. 10:1617-1630 (2000).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Cortex;  
 RX MEDLINE=20530913; PubMed=11076861;  
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
 RA Kono H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,  
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
 RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,  
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,  
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
 RT "RIKEN integrated sequence analysis (RISA) system-384-format  
 RT sequencing pipeline with 384 multicapillary sequencer";  
 RL Genome Res. 10:1757-1771 (2000).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Cortex;  
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,  
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,  
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohnato N., Okazaki Y.,  
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,  
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,  
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

RESULT 19  
 BAC31641



DR EMBL; AK043748; BAC31641.1; -  
SQ SEQUENCE 614 AA; 68168 MW; 66E2512463C21172 CRC64;  
Query Match 53.9%; Score 1675.5; DB 2; Length 614;  
Best Local Similarity 52.8%; Pred. No. 2.3e-117;  
Matches 306; Conservative 104; Mismatches 163; Indels 7; Gaps 4;  
QY 1 EDDIIATKNGKRGVGMVLTGCTVTAFLGIPYAPPLGLRFRKKPSLTKSDIMNATK 60  
DB 36 DPQLVAVRGGQALGIRLKAAPGVSAFLGIPFAEPVGSRRFMPPEKRWMSGLDATT 95  
QY 61 YANSCCONIDOSPFGHSEKMNPNNTLSEDCLYLWVTPAPKPKNAT-VLIWYGGGFG 119  
DB 96 FQNVCTGYVDTLYPGFEGTEKMNPNRRLSEDCLYLWVTPAPKPKNAT-VLIWYGGGFG 155  
QY 120 TGTSLHVDYDGFKLARVERVIVSMYRVGALPGNPEAGNNGLPDQALQWQ 179  
DB 156 SGAASLDVYDGRFLAQVGAVALVSMYRVGTFGLALPGSREAGVNGLDQRLALQWQ 215  
QY 180 KNTAAGGNPKSVTLFGESAGASVSILHLSPGSHSLFTTALIOGSFNAFWATSYEA 239  
DB 216 ENIAAFGGDPMSTVTLFGESAGASVGMHILSLPERSLFRHRAVLQSTPNMGMAVTSAGEA 275  
QY 240 RNRFLNIAKTGC---SRENETEIIKCLRNKDPQELILNFAVVPYGTPLSVNPGPTVD 295  
DB 276 RRRATLLARLVGCPGAGAGNDTELIACTRRPADLVDEHMHVLPQESIRFSGFVFPVD 335  
QY 296 GDFPLMDPDLIELGOKRKOIIVGNKDECTFLVYAGAPSGKDNISIRKESFOGSLK 355  
DB 336 GDFPLSDPEALINGDFODLQVLGVVKBESGYLVYVGPFSKDNISLRAOFLAGVR 395  
QY 356 IFFPGVSEFGKESILFYITDVAVDORPENYREALGDVGNDFICPALEPTKSESGN 415  
DB 396 IGPQASDLAEAVVLTITDMLHEDPHLMDASAVGVHNVCPVAQLAGRLAAGAR 455  
QY 416 AFYFFEHRSKSLPWPBMGVGMAGYEIEFVFGLEBRDNTYKAEILSRISVRMANFA 475  
DB 456 VVAIFEHRASTLTWPLMGVPGHYEIEFGLPLDPSLNTYTERIFAQILMKYMNFA 515  
QY 476 KYGNPNNTQNN-SISWVPEKSTEOKYLTLNTESTRITKLAQAOCRPWTSFFPVLEMTG 534  
DB 516 RTGPNPNRDSKSPQWPPYTTAAQOYVSLINKPLEVRGRLAAQCAFWNRLPLLSATD 575  
QY 535 NIDEAEWEMKAGFHRMNNYMMMDKNQFNDDYTSKESCVGL 574  
DB 576 TLDEAEKQAKAEFRMSSTYVHMKNQFDHY-SKQERGSGL 614  
RESULT 20  
BAC32595 PRELIMINARY; PRT: 614 AA.  
AC BAC32595:  
DT 14-APR-2004 (TrEMBLrel. 27, Created)  
DT 14-APR-2004 (TrEMBLrel. 27, Last sequence update)  
DT 14-APR-2004 (TrEMBLrel. 27, Last annotation update)  
DE Adult male corpora quadrigemina cDNA, RIKEN full-length enriched library, clone:H2303401.3 product:acetylcholinesterase, full insert  
DE sequence.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxId=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;  
RX MEDLINE=22354683; PubMed=12466851;  
RA The FANTOM Consortium,  
RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT Nature 420:563-573 (2002)."  
RL [2]  
RN SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;  
RX MEDLINE=21085660; PubMed=11217851;  
RA RIKEN FANTOM Consortium;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690(2001).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;  
RX MEDLINE=99279253; PubMed=10349636;  
RA Carninci P., Hayashizaki Y.;  
RT "High-efficiency full-length cDNA cloning.";  
RL Meth. Enzymol. 303:19-44(1999).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;  
RX MEDLINE=20499374; PubMed=11042159;  
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
RT prepare full-length cDNA libraries for rapid discovery of new genes.";  
RL Genome Res. 10:1617-1630(2000).  
RN [5]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;  
RX MEDLINE=20530913; PubMed=11076861;  
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
RA Kono H., Akiyama J., Nishi K., Kitanaui T., Tashiro H., Itoh M.,  
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
RA Yamamoto K., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
RA Fujitake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,  
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsumura S., Kawai J.,  
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
RT "RIKEN integrated sequence analysis (RISA) system-384-format  
RT sequencing pipeline with 384 multicapillary sequencer.";  
RL Genome Res. 10:1757-1771(2000).  
RN [6]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;  
RX MEDLINE=20530913; PubMed=11076861;  
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirokawa T.,  
RA Hori F., Imotani K., Ishii Y., Itoh M., Kigawa I., Kasubawa T.,  
RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,  
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
RA Nishi K., Nomura K., Numazaki R., Ohno M., Obatao N., Okazaki Y.,  
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,  
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,  
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AK046080; BAC32595.1; -  
SQ SEQUENCE 614 AA; 68168 MW; 66E2512463C21172 CRC64;  
Query Match 53.9%; Score 1675.5; DB 2; Length 614;  
Best Local Similarity 52.8%; Pred. No. 2.3e-117;  
Matches 306; Conservative 104; Mismatches 163; Indels 7; Gaps 4;  
QY 1 EDDIIATKNGKRGVGMVLTGCTVTAFLGIPYAPPLGLRFRKKPSLTKSDIMNATK 60  
DB 36 DPQLVAVRGGQALGIRLKAAPGVSAFLGIPFAEPVGSRRFMPPEKRWMSGLDATT 95  
QY 61 YANSCCONIDOSPFGHSEKMNPNNTLSEDCLYLWVTPAPKPKNAT-VLIWYGGGFG 119  
DB 96 FQNVCTGYVDTLYPGFEGTEKMNPNRRLSEDCLYLWVTPAPKPKNAT-VLIWYGGGFG 155  
QY 120 TGTSLHVDYDGFKLARVERVIVSMYRVGALPGNPEAGNNGLPDQALQWQ 179  
DB 156 SGAASLDVYDGRFLAQVGAVALVSMYRVGTFGLALPGSREAGVNGLDQRLALQWQ 215  
QY 180 KNTAAGGNPKSVTLFGESAGASVSILHLSPGSHSLFTTALIOGSFNAFWATSYEA 239  
DB 216 ENIAAFGGDPMSTVTLFGESAGASVGMHILSLPERSLFRHRAVLQSTPNMGMAVTSAGEA 275

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QY 240 RNNLTNLAKITGC-----SRNETETIKCLRNKDPQELINEARVVPYPTPLSNFGPTVD 295
DB 276 RRRATTLARLVGCPGAGAGNDTELACLRTPAQLVDHEMVLVQESIFRSEFVPVD 335
QY 296 GDBLTMDPDLLELQGFQKTKQILVGNKDEGTWFLVYAGPFSKDNNSIITRKEFOEGLK 355
DB 336 GDBLTMDPDLLELQGFQKTKQILVGNKDEGTWFLVYAGPFSKDNNSIITRKEFOEGLK 395
QY 356 IFPPGVSEFGKESILFHYTDWDDQRPENYREALGDVVDYNFICPALEFTKFSSEWKN 415
DB 396 IGVPGASDLAAVAVLHYTDMLHPEDPTHLRDAMSAYVGDHNVCPAQLAGLAQGAR 455
QY 416 APTFYFHHSSSKLPMPWGMVGHYEIEFVFGPLPERNDNTYKAEELISYIKRANRA 475
DB 456 VYAVIIFHHRASLTLPWLMGVPHGYEIEFVFGPLPERNDNTYKAEELISYIKRANRA 515
QY 476 KYGNPNETONN-STSWVFSTOCKYLLTNTESTRITMTKLRAOQCFWTSFFPKVLEMTG 534
DB 516 RTGDNDPDRSKSPQWPPYTTAAQYVSLKLEVRGRLAQTCAPMNRFLPKLSATD 575
QY 535 NIDEAEWEMKAGFHRNNNMWMDKQNPNDYTSKXESCVGL 574
DB 576 TLDEARQWKAFFHRMGSYVWVMKNQPDHY-SKQERCSDL 614

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## RESULT 21

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QY 09GKU6 PRELIMINARY; PRT; 349 AA.
ID 09GKU6
AC 01-MAR-2001 (TREMELREL. 16, Created)
DT 01-MAR-2001 (TREMELREL. 16, Last sequence update)
DT 01-OCT-2003 (TREMELREL. 25, Last annotation update)
DE Butyrylcholinesterase (fragment).
GN Name=ACHE;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxID=96823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21419000; PubMed=11528129;
RA Van Poucke M., Yexle M., Tugge C., Piumi F., Genet C.,
RT Van Zeveren A., Peelman L.J.;
RL "Integration of porcine chromosome 13 maps.";
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
DB EMBL: AF222914; AAC41127.1;
DR GO: GO:0003824; F:catalytic activity; IEA.
DR GO: GO:0004104; F:cholinesterase activity; IEA.
DR InterPro: IPR002018; CarbesteraseB.
DR InterPro: IPR000997; Cholinesterase.
DR InterPro: IPR000379; Ser_estrs.
DR Pfam: PF00135; Coesterase; 1.
DR PRINTS: PR00878; CHOLINESTRASE.
DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
FT NON_TER 1
FT NON_TER 349
SQ SEQUENCE 349 AA; 39061 MW; D66354B14725B58 CRC64;

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Query Match 53.8%; Score 1674; DB 2; Length 349;
Best Local Similarity 91.4%; Pred. No. 1,4e-117;
Matches 319; Conservative 6; Mismatches 24; Indels 0; Gaps 0;

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QY 113 IYGGFPGTGTSSLHYDDGFLARVERVYVSNMNVGALGFALPGNEARQNGMGLPQQ 172
DB 1 IYGGFPGTGTSSLHYDDGFLARVERVYVSNMNVGALGFALPGNEARQNGMGLPQQ 60
QY 173 LALOWVOKKIAAFGNGPKSVTLFGESAGASVSLHLSPGSHSLFTRAILGSGSTNAPWA 232
DB 61 LALOWVOKKIAAFGNGPKSVTLFGESAGASVSLHLSPGSHSLFTRAILGSGSTNAPWA 120
QY 233 VTSLYEARNTLTLAKITGCSRENETEIIKCLRNKDPQELINEARVVPYPTPLSNFGP 292

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DB 121 VTSLYEARNTLTLAKITGCSRENETEIIKCLRNKDPQELINEARVVPYPTPLSNFGP 180
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DB 181 TYDGFPLDMDDILLELQGFQKTKQILVGNKDEGTWFLVYAGPFSKDNNSIITRKEFOE 240
QY 353 GLKIFPPGVSEFGKESILFHYTDWDDQRPENYREALGDVVDYNFICPALEFTKFSSEW 412
DB 241 GLKIFPPGVSEFGKESILFHYTDWDDQRPENYREALGDVVDYNFICPALEFTKFSSEW 300
QY 413 GNNAFYYFHHSSSKLPMPWGMVGHYEIEFVFGPLPERNDNTYKAE 461
DB 301 GNNAFYYFHHSSSKLPMPWGMVGHYEIEFVFGPLPERNDNTYKAE 349

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## RESULT 22

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ACCS FELCA STANDARD; PRT; 611 AA.
ID ACES_FELCA
AC 062763; 062762;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Acetylcholinesterase precursor (BC 3.1.1.7) (ACHE).
GN Name=ACHE;
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RX MEDLINE=20334351; PubMed=10874122;
RA Bartels C.F., Xie W., Miller-Lindholm A.K., Schopfer L.M.,
RT Lockridge O.;
RL "determination of the DNA sequences of acetylcholinesterase and
butyrylcholinesterase from cat and demonstration of the existence of
both in cat plasma.";
RT Biochem. Pharmacol. 60:479-487(2000).
CC -1- FUNCTION: Rapidly hydrolyzes choline released into the synapse.
CC -1- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.
CC -1- SUBUNIT: Interacts with PRIMA1. The interaction with PRIMA1 is
required to anchor it to the basal lamina of cells and organized
into tetramers (By similarity). Isoform H generates multiple structures,
dimers; disulfide linked. Isoform T generates multiple structures,
ranging from monomers and dimers to collagen-tailed and
hydrophobic-tailed forms, in which catalytic tetramers are
associated with anchoring proteins that attach them to the basal
lamina or to cell membranes. In the collagen-tailed forms, isoform
T subunits are associated with a specific collagen, COLQ, which
triggers the formation of isoform T tetramers, from monomers and
dimers.
CC -1- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
Name=T;
IsoId=O62763-1; Sequence=displayed;
Name=H;
IsoId=O62763-2; Sequence=VSP_001456;
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to jlicense@isb-sib.ch).
CC EMBL: AF053485; AAC08995.1; -.
DB EMBL: AF053485; AAC08996.1; -.
DR HSSP: P22303; 1F8U.
DR InterPro: IPR002018; CarbesteraseB.
DR InterPro: IPR000997; Cholinesterase.
DR InterPro: IPR000379; Ser_estrs.
DR Pfam: PF00135; Coesterase; 1.
DR

```







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FT DISULFID 561 561 Interchain.
FT CARBOHYD 83 83 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 440 440 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 481 481 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 557 557 N-linked (GlcNAc...) (Potential).
FT LIPID 567 567 GPI-anchor amidated serine.
FT VARSPLIC 560 590 ACDELSSGSGTSSKGIIFVLFSTIYLIFY -> ETIDEA
FT VARSPLIC 560 590 ERQMKTEPHRWSYMMHMKQFDQYSRHENCHEL (in
FT isoform 1).
FT VARSPLIC 560 590 /FTid=VSP_001461.
FT VARSPLIC 560 590 ACDELSSGSGTSSKGIIFVLFSTIYLIFY -> GNVFAF
FT HMKVRPRPKATYHRCVIVAHLLSLPTASDVPRLASKWM
FT AHSDPLCSKRCWESWGRIL (in isoform 3).
FT /FTid=VSP_001462.
SQ SEQUENCE 590 AA; 66744 MW; 73FAC284C9784F25 CRC64;

Query Match 53.0%; Score 1649; DB 1; Length 590;
Best Local Similarity 53.5%; Pred. No. 2,1e-115;
Matches 285; Conservative 105; Mismatches 143; Indels 0; Gaps 0;

QY 1 EDDIIATKNGKXVGMNLTVEGTVTAFLGIPYAQPLGLRFRKKQSLTKMSDINNAIK 60
DB DSELIVNTKSGKWRTRIPVLSHISAFLGIPFAEPVGMRRPRRPPKPKMGSVGNWAST 86
QY 61 YANSCCNIDQSPFGFSGEMWNPNTLSDCLYINWIPAPKPKXATVLIWYGGGFOT 120
DB YPNNCQOYVDEQFPFGSGEMWNPNTLSDCLYINWIPAPKPKXATVLIWYGGGFOT 146
QY 121 GTSILHYDGGFLARVERVIVSNMYRVGALGFALPGNEAPQNMGLFDQOLALQWVOK 180
DB GSSTLDVYNGKYLATYEVIVLSIYVGAAGFLAHGSOEAPENWGILLDQRMALQWVHD 206
QY 147 GSSTLDVYNGKYLATYEVIVLSIYVGAAGFLAHGSOEAPENWGILLDQRMALQWVHD 206
QY 181 NIAAFGNPKSVTLFGESAGASVSLHLSPGSHSLFTRAILOSGSTNAPMAVTSIYEAR 240
DB NIQFPGGDPKTVTLFGESAGASVGMHILSPGSRDLFRRAILOSGSPNCPMASVSAEGR 266
QY 207 NRTLNIAKLTCGSRNENETIICKLRNDPOEIIINBAFVVPYGTPLSVNFGPTVDGDLT 300
DB RRAVELRKNLNCNLNSDEDLIQCLREKKPQELIIVEMNVLPFDSIRPFSFVVIDGEFFP 326
QY 241 DMPDILLETGQFKTQILVGNKDEGTWFLVYGAAGFSKDNNSIITKEFOEGLKIFPG 360
DB TSLSMNLNAGNFKKTQILVGNKDEGSFLLYGAPGFSKDSKISREDFMSGVKLSVPH 386
QY 327 TSLSMNLNAGNFKKTQILVGNKDEGSFLLYGAPGFSKDSKISREDFMSGVKLSVPH 386
QY 361 VSEFGKESILFHYTDWVDQRPENTREALGVVGDYINFCALFTKKSEMGNNAFYY 420
DB ANDGLDAVTLQYTDMDNDNGIKNRDGLDDIVGDHNVICPLMHFVNKYTFKNGTLYLF 446
QY 387 FEHSSSKLPWPEMNGVMHGEIEFVGLPLERRDNYTAAEILSRSIYKRWANFAKYGNP 480
DB FNRHSNLYWPEMNGVHGEIEFVGLPLVKEINLYTAEELASRIIMHYATFAKTGNP 506
QY 447 FNRHSNLYWPEMNGVHGEIEFVGLPLVKEINLYTAEELASRIIMHYATFAKTGNP 506
QY 481 NETONNSTSWPVFKSTEQKYLTLNTESTRIMTKLAQOCRFWTSFPPVLENT 533
DB NEPHSGSKMPLFTTKEQKFDLNTPEPIKHQRLRVQMCVFWNGFLPLLNAT 559
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Search completed: January 6, 2005, 09:59:42  
Job time : 203 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 6, 2005, 09:50:36 ; Search time 43 Seconds  
(without alignments)  
1284.382 Million cell updates/sec

Title: US-09-748-739a-2\_COPY\_29\_602

Perfect score: 3110

Sequence: 1 EDDIIITATKNGKVGKGNLTV.....MDWKQNPDYTSKSKSCVGL 574

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : PIR\_79:\*

1: p1r1:\*

2: p1r2:\*

3: p1r3:\*

4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3096	99.5	602	1	cholinesterase (EC
2	2843	91.4	581	2	cholinesterase (EC
3	2521	81.1	603	2	cholinesterase (EC
4	1785.5	57.4	596	1	cholinesterase (EC
5	1784.5	57.4	599	1	cholinesterase (EC
6	1689	54.3	614	2	cholinesterase (EC
7	1678.5	54.0	614	2	cholinesterase (EC
8	1675.5	53.9	614	2	cholinesterase (EC
9	1639	52.7	584	2	cholinesterase (EC
10	1636.5	52.6	583	2	cholinesterase (EC
11	1455.5	46.8	767	2	cholinesterase (EC
12	1142	36.7	620	2	cholinesterase (EC
13	1070.5	34.4	637	2	cholinesterase (EC
14	1044	33.6	746	2	cholinesterase (EC
15	1040.5	33.5	691	2	cholinesterase (EC
16	1030.5	33.1	664	2	cholinesterase (EC
17	1012.5	32.6	602	2	cholinesterase (EC
18	948	30.5	629	2	cholinesterase (EC
19	937	30.1	629	2	cholinesterase (EC
20	930	29.9	607	2	cholinesterase (EC
21	893	28.7	532	2	cholinesterase (EC
22	754	24.2	532	2	cholinesterase (EC
23	753	24.2	532	2	cholinesterase (EC
24	732	23.5	599	2	cholinesterase (EC
25	729	23.4	597	2	cholinesterase (EC
26	728.5	23.4	559	1	cholinesterase (EC
27	726	23.3	612	2	cholinesterase (EC
28	724	23.3	141	2	cholinesterase (EC
29	721	23.2	141	2	cholinesterase (EC

30	721	23.2	141	2	cholinesterase (EC
31	718.5	23.1	561	2	cholinesterase (EC
32	715	23.0	554	2	cholinesterase (EC
33	711	22.9	745	2	cholinesterase (EC
34	708.5	22.8	565	2	cholinesterase (EC
35	707	22.7	557	2	cholinesterase (EC
36	701.5	22.6	557	2	cholinesterase (EC
37	697.5	22.4	567	1	cholinesterase (EC
38	696.5	22.4	562	2	cholinesterase (EC
39	694.5	22.3	561	2	cholinesterase (EC
40	690.5	22.2	566	2	cholinesterase (EC
41	690	22.2	549	2	cholinesterase (EC
42	689	22.2	549	2	cholinesterase (EC
43	680.5	21.9	561	2	cholinesterase (EC
44	675.5	21.7	561	2	cholinesterase (EC
45	666	21.4	956	2	cholinesterase (EC
46	651	20.9	554	1	cholinesterase (EC
47	649	20.9	540	2	cholinesterase (EC
48	634	20.4	2769	1	cholinesterase (EC
49	631	20.3	967	1	cholinesterase (EC
50	627	20.2	540	2	cholinesterase (EC
51	623.5	20.0	593	1	cholinesterase (EC
52	619	19.9	539	2	cholinesterase (EC
53	614	19.4	2767	1	cholinesterase (EC
54	603.5	19.4	562	2	cholinesterase (EC
55	595	19.1	564	1	cholinesterase (EC
56	594	19.1	489	2	cholinesterase (EC
57	585.5	18.8	583	2	cholinesterase (EC
58	585	18.8	505	2	cholinesterase (EC
59	583	18.7	552	2	cholinesterase (EC
60	582.5	18.7	554	2	cholinesterase (EC
61	582.5	18.7	557	2	cholinesterase (EC
62	574.5	18.5	564	2	cholinesterase (EC
63	556	17.9	547	2	cholinesterase (EC
64	554.5	17.8	562	2	cholinesterase (EC
65	553	17.8	548	2	cholinesterase (EC
66	546.5	17.6	550	1	cholinesterase (EC
67	540.5	17.4	570	2	cholinesterase (EC
68	538.5	17.3	730	2	cholinesterase (EC
69	531.5	17.1	502	2	cholinesterase (EC
70	528.5	17.0	578	2	cholinesterase (EC
71	528.5	17.0	658	2	cholinesterase (EC
72	526	16.9	543	2	cholinesterase (EC
73	522	16.8	565	2	cholinesterase (EC
74	520.5	16.7	545	2	cholinesterase (EC
75	520	16.7	540	2	cholinesterase (EC
76	512	16.5	540	2	cholinesterase (EC
77	510	16.4	571	2	cholinesterase (EC
78	509.5	16.4	798	2	cholinesterase (EC
79	508	16.3	540	2	cholinesterase (EC
80	507	16.3	535	2	cholinesterase (EC
81	499.5	16.1	549	2	cholinesterase (EC
82	497	16.0	578	2	cholinesterase (EC
83	491	15.8	453	2	cholinesterase (EC
84	482.5	15.5	564	2	cholinesterase (EC
85	482	15.5	544	2	cholinesterase (EC
86	481	15.5	563	1	cholinesterase (EC
87	479	15.4	544	2	cholinesterase (EC
88	477	15.3	548	2	cholinesterase (EC
89	476	15.3	544	2	cholinesterase (EC
90	476	15.3	544	2	cholinesterase (EC
91	474	15.2	544	2	cholinesterase (EC
92	473	15.2	544	2	cholinesterase (EC
93	473	15.2	544	2	cholinesterase (EC
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95	473	15.2	548	2	cholinesterase (EC
96	472	15.2	544	2	cholinesterase (EC
97	471.5	15.2	553	2	cholinesterase (EC
98	470	15.1	544	2	cholinesterase (EC
99	468	15.0	544	2	cholinesterase (EC
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Qy 2 DDIITATKNGKVGKMLTVFGGTVTAFLGIFVYAOPLGRLPKKQSLTKMSDIMNATK 61  
 Db 9 EDVLIITTKNGRIRGINLPVFGGTVAFLGIPYAOPLGRLPKKQSLTKMSDIMNATK 68  
 Qy 62 ANSCCONIDQSPFGHSEMMNPNTDLSBDCLYLNWIPAPKPKNATVLIWYGGGFQT 121  
 Db 69 ANSCCONIDQSPFGHSEMMNPNTDLSBDCLYLNWIPAPKPKNATVMIWYGGGFQT 128  
 Qy 122 TSSLHYVDGKFLARVERIVVSNMYRVGALGFLAPGNPAQNMGLFDQQLALQWVOK 181  
 Db 129 TSSLQVYDGKFLARVERIVVSNMYRVGALGFLAPGNPAQNMGLFDQQLALQWVOK 188  
 Qy 182 IAAFGNPKSVTLFGESAGAASVSLHLSPGSHSLFTRAILQSGSFNAFPAVTSLEYARN 241  
 Db 189 IAAFGNPKSVTLFGESAGAASVSLHLSPGSHSLFTRAILQSGSFNAFPAVTSLEYARN 248  
 Qy 242 RTLNLAKLTGCSRENTEIICLRNKDPOEILLNEAFVVPYGTPLSVNFGPTVDGDFLT 301  
 Db 249 RTLNLAKLTGCSRENTEIICLRNKDPOEILLNEAFVVPYGTPLSVNFGPTVDGDFLT 308  
 Qy 302 MPDILLELGQFKTQIILVGNKDEGTWFLVYGAQPGFSKONNSITTRKFOGGLKIFPGV 361  
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 Qy 362 SEFGKESILFHYTDMVDQRENTREALGDVVDYVFCPALFETKCFSEMGNAFFYYF 421  
 Db 369 SEFGKESILFHYTDMVDQRENTREALGDVVDYVFCPALFETKCFSEMGNAFFYYF 428  
 Qy 422 EHRSSKLPMPWEMVGMHGYEIEFVFGPLERRDNTYKAEILSRISYKMANFAKYGNP 481  
 Db 429 EHRSSKLPMPWEMVGMHGYEIEFVFGPLERRDNTYKAEILSRISYKMANFAKYGNP 488  
 Qy 482 ETONNSTWMPVKSTBOCYLTINTESTRIMTKLRADQOCFMTSPFKYLEMTGNIDEAEW 541  
 Db 489 ETONNSTWMPVKSTBOCYLTINTESTRIMTKLRADQOCFMTSPFKYLEMTGNIDEAEW 548  
 Qy 542 EMKAGFHRMNNYMDWKQFNPDYTSKESCVG 573  
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## RESULT 3

S70849  
 N:Alternate names: butyrylcholine esterase  
 C:Species: Mus musculus (house mouse)  
 C/Date: 28-Oct-1996 #sequence revision 08-Nov-1996 #text\_change 09-Jul-2004  
 C/Accession: S70849; S15680; A39768  
 R:Taylor, P.  
 A:Reference number: S70849  
 A:Accession: S70849  
 A:Molecule type: nucleic acid  
 A:Residues: 1-603 <TRY>  
 A:Cross-references: UNIPROT:Q03311; EMBL:M99492; NID:q191579; PIDN:AAA37328.1; PID:q1915  
 R:Schumacher, T.L.; Camp, S.; Li, Y.; Ekstrom, T.J.; Newton, M.; Taylor, P.  
 A:Title: Molecular cloning of mouse acetylcholinesterase: tissue distribution of alterna  
 A:Reference number: JH0314; MUID:90380429; PMID:2400605  
 A:Accession: S15680  
 A:Status: nucleic acid sequence not shown  
 A:Molecule type: nucleic acid  
 A:Residues: 30-128, 'P', 130-603 <RAC>  
 A:Cross-references: EMBL:M99492  
 R:Appagana, M.; Chatterjee, A.; Masson, P.; Newton, M.; Vaughan, T.A.; Bartels, C.F.; Nog  
 J. Biol. Chem. 265, 6966-6974, 1991  
 A:Title: Use of the polymerase chain reaction for homology probing of butyrylcholinester  
 A:Reference number: A39768; MUID:91201348; PMID:2016308  
 A:Accession: A39768  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 97-128, 'P', 130-237 <ARP>

C:Superfamily: cholinesterase; cholinesterase homology  
 C:Keywords: carboxylic ester hydrolase; glycoprotein  
 F:57-557/Domain: cholinesterase homology <CHB>

Query Match 81.1%; Score 2521; DB 2; Length 603;  
 Best Local Similarity 80.5%; Pred. No. 3.5e-185;  
 Matches 462; Conservative 47; Mismatches 65; Indels 0; Gaps 0;

Qy 1 EDDIITATKNGKVGKMLTVFGGTVTAFLGIPYAOPLGRLPKKQSLTKMSDIMNATK 60  
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 Qy 61 YANSCCONIDQSPFGHSEMMNPNTDLSBDCLYLNWIPAPKPKNATVLIWYGGGFQT 120  
 Db 90 YANSCCONIDQSPFGHSEMMNPNTDLSBDCLYLNWIPAPKPKNATVMIWYGGGFQT 149  
 Qy 121 TSSLHYVDGKFLARVERIVVSNMYRVGALGFLAPGNPAQNMGLFDQQLALQWVOK 180  
 Db 150 TSSLHYVDGKFLARVERIVVSNMYRVGALGFLAPGNPAQNMGLFDQQLALQWVOK 209  
 Qy 181 IAAFGNPKSVTLFGESAGAASVSLHLSPGSHSLFTRAILQSGSFNAFPAVTSLEYARN 240  
 Db 210 IAAFGNPKSVTLFGESAGAASVSLHLSPGSHSLFTRAILQSGSFNAFPAVTSLEYARN 269  
 Qy 241 RTLNLAKLTGCSRENTEIICLRNKDPOEILLNEAFVVPYGTPLSVNFGPTVDGDFLT 300  
 Db 270 RTLNLAKLTGCSRENTEIICLRNKDPOEILLNEAFVVPYGTPLSVNFGPTVDGDFLT 329  
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 Db 330 MPDILLELGQFKTQIILVGNKDEGTWFLVYGAQPGFSKONNSITTRKFOGGLKIFPGV 389  
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 Db 390 VSEFGKESILFHYTDMVDQRENTREALGDVVDYVFCPALFETKCFSEMGNAFFYYF 449  
 Qy 422 EHRSSKLPMPWEMVGMHGYEIEFVFGPLERRDNTYKAEILSRISYKMANFAKYGNP 480  
 Db 450 EHRSSKLPMPWEMVGMHGYEIEFVFGPLERRDNTYKAEILSRISYKMANFAKYGNP 509  
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 Db 510 NETONNSTWMPVKSTBOCYLTINTESTRIMTKLRADQOCFMTSPFKYLEMTGNIDEAE 569  
 Qy 541 EMKAGFHRMNNYMDWKQFNPDYTSKESCVG 574  
 Db 570 EMKAGFHRMNNYMDWKQFNPDYTSKESCVG 603

## RESULT 4

ACRYE  
 N:Alternate names: acetylcholinesterase, asymmetric form  
 C:Species: Torpedo californica (Pacific electric ray)  
 C/Date: 17-Mar-1997 #sequence revision 08-Nov-1996 #text\_change 09-Jul-2004  
 C/Accession: A00773; A60820; B31962; A23902; S15677  
 R:Schumacher, M.; Camp, S.; Maule, Y.; Newton, M.; Macphie-Quigley, K.; Taylor, S.S.; F  
 Nature 319, 407-409, 1986  
 A:Title: Primary structure of Torpedo californica acetylcholinesterase deduced from its c  
 A:Reference number: A00773; MUID:86118676; PMID:3753747  
 A:Accession: A00773  
 A:Molecule type: mRNA  
 A:Residues: 'NS', 11-596 <SCH>  
 A:Cross-references: UNIPROT:P04058; GB:X03439; NID:g64389  
 A:Experimental source: electric organ  
 A>Note: parts of this sequence, including the amino and carboxyl ends of the mature prote  
 R:Schumacher, M.; Camp, S.; Maule, Y.; Newton, M.; Macphie-Quigley, K.; Taylor, S.S.; F  
 Fed. Proc. 45, 2976-2981, 1986  
 A:Title: Primary structure of acetylcholinesterase: implications for regulation and funct  
 A:Reference number: A60820; MUID:87054662; PMID:3536598  
 A:Accession: A60820  
 A:Status: nucleic acid sequence not shown  
 A:Molecule type: mRNA

A:Residues: 22-596 <SC2>  
 R:Schumacher, M.; Maulet, Y.; Camp, S.; Taylor, P.  
 J. Biol. Chem. 263, 18979-18987, 1988  
 A:Title: Multiple messenger RNA species give rise to the structural diversity in acetylcholinesterase  
 A:Reference number: A92701; MUID:8906695; PMID:3198606  
 A:Accession: A31962  
 A:Molecule type: mRNA  
 A:Residues: 1-23 <SC3>  
 A:Cross-references: EMBL:X03439; NID:964439  
 A:Experimental source: clones AChE-11 and AChE-18  
 A:Note: revision to sequence A00773  
 A:Accession: B31962  
 A:Molecule type: DNA  
 A:Residues: 439-565 <SC4>  
 A:Cross-references: CB:X03439; NID:964389  
 A:Experimental source: clone AChE-1  
 R:MacPhee-Quigley, K.; Taylor, P.; Taylor, S.  
 J. Biol. Chem. 260, 12185-12189, 1985  
 A:Title: Primary structures of the catalytic subunits from two molecular forms of acetylcholinesterase  
 A:Reference number: A23902; MUID:86008285; PMID:3900071  
 A:Accession: A23902  
 A:Molecule type: protein  
 A:Residues: 22, 'B', 24-45; 214-237 <MAC>  
 A:Note: active site Ser identification  
 R:Kreienkamp, H.U.; Weise, C.; Raba, R.; Aavikkaar, A.; Hucho, F.  
 Proc. Natl. Acad. Sci. U.S.A. 88, 6117-6121, 1991  
 A:Title: Anticatalytic substrates of the catalytic center of acetylcholinesterase from Torpedo marmorata  
 A:Reference number: A41117; MUID:91296772; PMID:2068091  
 A:Accession: B41117  
 A:Molecule type: protein  
 A:Residues: 100-108 <KRE>  
 A:Note: substrate binding site  
 R:Maulet, Y.; Camp, S.; Gibney, G.; Rachinsky, T.L.; Ekstrom, T.J.; Taylor, P.  
 Neuron 4, 289-301, 1990  
 A:Title: Single gene encodes glycopospholipid anchored and asymmetric acetylcholinesterase  
 A:Reference number: P50113; MUID:9016618; PMID:2306366  
 A:Accession: S15677  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 557-596 <MAU>  
 A:Cross-references: EMBL:X56516  
 R:MacPhee-Quigley, K.; Vedvick, T.S.; Taylor, P.; Taylor, S.S.  
 J. Biol. Chem. 261, 13565-13570, 1986  
 A:Title: Profile of the disulfide bonds in acetylcholinesterase  
 A:Reference number: A43099; MUID:87008586; PMID:3759980  
 A:Contents: annotation; disulfide bonds  
 R:Stussman, J.L.; Harel, M.; Silman, I.  
 submitted to the Brookhaven Protein Data Bank, October 1991  
 A:Reference number: A50061; PDB:1ACB  
 A:Contents: annotation; X-ray crystallography, 2.8 angstroms, residues 26-481, 511-555 of R:Stussman, J.L.; Harel, M.; Frolow, F.; Oefner, C.; Goldman, A.; Tokar, L.; Silman, I.  
 Science 253, 872-879, 1991  
 A:Title: Atomic structure of acetylcholinesterase from Torpedo californica: a prototypic AChE  
 A:Reference number: A43098; MUID:91343928; PMID:1678899  
 A:Contents: annotation; X-ray crystallography, 2.8 angstroms, residues 26-481, 511-555 of C:Comment: Synapses usually contain this 11S (asymmetric) form of cholinesterase with a holoenzyme occurs on the outer surfaces of cell membranes, including those of erythrocytes. C:Complex: 11S form is disulfide linked homodimer; 18S form is homotetramer, a dimer of C:Function:  
 A:Description: hydrolyzes acetylcholine to choline and acetate  
 A:Pathway: neurotransmitter degradation  
 C:Superfamily: cholinesterase; cholinesterase homology  
 C:Keywords: alternative splicing; carboxylic ester hydrolase; glycoprotein; membrane protein  
 F:1-21/Domains: signal sequence #status predicted <SIG>  
 F:22-596/Product: acetylcholinesterase, 11S form #status experimental <MAT>  
 F:51-551/Domains: cholinesterase homology <CHE>  
 F:80-478, 553/Binding site: carbonyl (Asn) (covalent) #status predicted  
 F:80-478, 553/Binding site: carbonyl (Asn) (covalent) #status experimental  
 F:105/Binding site: substrate (Trp) #status experimental  
 F:221/Active site: Ser #status experimental  
 F:348, 461/Active site: Glu, His #status predicted  
 F:437/Binding site: carbonyl (Asn) (covalent) #status experimental  
 F:593/Disulfide bonds: interchain #status experimental

Query Match 57.4%; Score 1785.5; DB 1; Length 596;  
 Best Local Similarity 54.0%; Pred. No. 8,4e-129;  
 Matches 309; Conservative 109; Mismatches 153; Indels 1; Gaps 1;  
 3 DIITATKNGKVGKMLTYFGGTVAFLGIPYAPQPLGRLRRKPKQSLTKWSDINWATKTA 62  
 26 ELIVNTKSGKVMGTVPVLSHISAFGLIPFAEPVPVGMRRFRPDPKRWGVMASVTP 85  
 63 NSCCQNIIDSPFGFSGSEMMNPNTLSEDCLYANWIPAPKPKATVLIWTVGGGFGTGT 122  
 86 NNQOQYVDQFPFGSGSEMMNPNTLSEDCLYANWIPAPKPKATVLIWTVGGGFGTGT 145  
 123 SSILHYDGFKLARVERVIVSNMRYVGLGFLALPQNPAPQNMGLPQQLALQWVQXNI 182  
 146 STLDVYNGKYLAVTEEVVLSLYVGAAGFLALHSGDEAPFNVGLDQRMALQWVHDI 205  
 183 AAFGNPKSVTLFGSAGAASTVLSLHSGSHSLTRALHSGSNAPPAVATSLYEAAR 242  
 206 QFPGDPTKVTITFGSAGAASTVLSLHSGSHSLTRALHSGSNAPPAVATSLYEAAR 265  
 243 TYNLAATGCSRENETEIKCLRNDPOBILNEAFVVPYGTPLSVNFGPTVDSFLTDM 302  
 266 AVELGNLNCNLSDELHCLREKKPQBLIVEMVLPFDSIRFSPVVIDGEFFPS 325  
 303 PDILLELQPKTKQILVGNKDEGTWFLVYGAAGFSKDNNSITTRKFOGLKIFPPGV 362  
 326 LBSMLNSGNPKTKQILVGNKDEGTWFLVYGAAGFSKDNNSITTRKFOGLKIFPPGV 385  
 363 EFKESILHYDWDVDDQPEYRRLGVDVNFICALEFTKFSKGNAPPYE 422  
 386 DLGLDVTLYDVTWMDNNGIKRDLIDVGHVTCPLMFVNKTYFGGTYLYFN 445  
 423 HRSSKLPFPMGVMGVEIEFVGLPLERBDNYTKAEILSRSLVKEWNAFYKGNPE 482  
 446 HRASNLVPEBMGVHIGYIEFVGLPLERBDNYTKAEILSRSLVKEWNAFYKGNPE 505  
 483 TONNSTWPFVSTKQKYLTLNTESTRIMTKLPAQOCRTWTFPPVLEMTGNIDAE 542  
 506 PHSQSKMPLFTTKQKFLDLNTEPMKQRLRQVQCVFQWQFLPLNATEITDAERQ 565  
 543 WKAGFRNNVMDKQFNQDYSKESQVGL 574  
 566 WKTEFRMSVYMHMKNQFDHY-SRHSQAEI 596  
 RESULT 5  
 A38868  
 acetylcholinesterase (EC 3.1.1.7) precursor - marbled electric ray  
 C:Species: Torpedo marmorata (marbled electric ray)  
 C>Date: 23-Apr-1993 #sequence revision 15-Nov-1996 #text change 09-Jul-2004  
 C:Accession: A38868; A29682; S15696; A25650  
 R:Massoulié, J.; Bon, S.  
 submitted to the EMBL Data Library, June 1992  
 A:Reference number: A38868  
 A:Accession: A38868  
 A:Molecule type: mRNA  
 A:Residues: 1-599 <MAS>  
 A:Cross-references: UNIPROT:P07692; EMBL:X05497; NID:964414; PIDN:CA29047.1; PID:964415  
 R:Sikora, J.L.; Krejci, E.; Massoulié, J.  
 EMBO J. 6, 1865-1873, 1987  
 A:Title: cDNA sequences of Torpedo marmorata acetylcholinesterase: primary structure of t  
 A:Reference number: A29682; MUID:88004392; PMID:2820709  
 A:Accession: A29682  
 A:Molecule type: mRNA  
 A:Residues: 1-40, 'G', 42-226, 'G', 228-272, 'G', 274-284, 'E', 286-420, 'N', 422-599 <SIR>  
 A:Cross-references: EMBL:X05497  
 R:Sikora, J.L.; Duval, N.; Anselmet, A.; Bon, S.; Krejci, E.; Legay, C.; Osterlund, M.;  
 EMBO J. 7, 2983-2993, 1988  
 A:Title: Complex alternative splicing of acetylcholinesterase transcripts in Torpedo elec  
 A:Reference number: S01293; MUID:89030590; PMID:3181125  
 A:Accession: S15696  
 A:Molecule type: mRNA

A:Residues: 526-599 <S12>  
A:Cross-references: EMBL:X13172; NID:964416; PIDN:CAA31570.1; PID:964417  
A:Experimental source: clone pACHE2  
R:Bon, S.; Chang, J.Y.; Strosberg, A.D.  
FEBS Lett. 209, 206-212, 1986  
A:Title: Identical N-terminal peptide sequences of asymmetric forms and of low-salt-soluble acetylcholinesterase.  
A:Reference number: A91370; MUID:87080761; PMID:3792544  
A:Accession: A25650  
A:Molecule type: protein  
A:Residues: 25-40, 'G', 42-47 <BON>  
A:Gene: ACHB  
A:Function:  
A:Description: hydrolyzes acetylcholine to choline and acetate  
A:Pathway: neurotransmitter degradation  
C:Superfamily: cholinesterase; cholinesterase homology  
C:Keywords: alternative splicing; carboxylic ester hydrolase; glycoprotein; neurotransmitter; signal sequence #status predicted <SIG>  
F:1-24/Domain: signal sequence #status predicted <SIG>  
F:25-599/Product: acetylcholinesterase #status predicted <MAT>  
F:54-554/Domain: cholinesterase homology <CH>  
F:83,440,481,557/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:91-118,278-289,426-545/Disulfide bonds: #status predicted  
F:224,351,464/Active site: Ser, Glu, His #status predicted  
F:596/Disulfide bonds: interchain #status predicted

Query Match 57.4%; Score 1784.5; DB 1; Length 599;  
Best Local Similarity 53.8%; Pred. No. 1e-128; Indels 1; Gaps 1;  
Matches 309; Conservative 111; Mismatches 153;

1 EDDIIITKNGKRGKGMNLTVPFGTVAFLGIPYAPPLGRLRFRKPKQSLTKMSDINWATK 60  
27 DSELIVNTKSGKMTKRTIPVLSHISAFGLGFPAEPVGMRRPRRPPKPKWGSVWNAAT 86  
61 YANSCCONIDQSPFGFGSEMMNPTDLSDDCLYNWIPAKPKKAT-VLIWYGGF 120  
87 YPNNCQYVDEQFPGFPGSEMMNPTDLSDDCLYNWIPAKPKKAT-VLIWYGGF 146  
121 GTSSTLHYDQKFLARVERVIVSMNRYGALGFLALPGNPAAGMGLDQRLALQWV 180  
147 GSSTLDYNGKTYLTYEVLVLSYRVGAFGLALHSGSAPAGMGLDQRLALQWV 206  
181 NIAFAGNPKSVTLFGESAGAASVLSLSPGSHLFTTRAILQSGSFNAPAWATSLYE 240  
207 NIFPGDPRKTVTLFGESAGASVGMHLSFGSDLRRAILQSGSNCMAVSVAEGR 266  
241 NRTLNTAKLTGCSRENETEIIKCLRNKPOEILINAEFVVPYGTPLSVNFGPTVDG 300  
267 RRAVELRRNINCNLNSDEDLIQCLREKPPQELIDVENWVLPFDSIFRFSFVPI 326  
301 DMEIDLLELQFKKTOILVGNKDEGFWPLVYGA RGSKDNNSITRKEFOEGLKIF 360  
327 TSLSEMLNANPKTKQILLGVNKGSGFPLLYGAPGSKSEKISREDFNPGVKS 386  
361 VSEFGKESILFHYTDWVDQRPENYREALGDVVDYVFCPALFTFKKFSWGNNAFF 420  
387 ANDLGDAVLTQITDMDNDNGIKNRDGLDIVGDHVICPLMFVAKYTKFGYGLY 446  
447 FNRASLTVPEWVGVIHGYEIEFVGLPLVKEILNTYAEBAALSRRIMHWATPAK 506  
481 NEONNSTSWPVFSTQKTLTNTSTRIMTKLRAQOCRFWTSFPFKVLEMTGNID 540  
507 NEPSQSKWPLFTTKQKPIDLNTEBPIKYHQRILRVQWCVFWNDFPKLNTAET 566  
541 MEMKAGFRHNNVMDKQNFNDYTSKESCVGL 574  
567 RQKTEFHRSSTYMHKNOFDQ-SRHNCAL 599

RESULT 6  
A39256

acetylcholinesterase (EC 3.1.1.7) precursor, brain splice form - human  
C:Species: Homo sapiens (man)  
C:Date: 18-Oct-1991 #sequence\_revision 18-Oct-1991 #text\_change 09-Jul-2004  
A:Accession: A39256; S03959  
R:Soreq, H.; Ben-Aziz, R.; Prody, C.A.; Seidman, S.; Gnatt, A.; Neville, L.; Lieman-Hurw, Proc. Natl. Acad. Sci. U.S.A. 87, 9688-9692, 1990  
A:Title: Molecular cloning and construction of the coding region for human acetylcholinesterase.  
A:Reference number: A39256; MUID:91088577; PMID:2263619  
A:Accession: A39256  
A:Molecule type: mRNA  
A:Residues: 1-614 <SOR>  
A:Cross-references: UNIPROT:P22303; GB:M55040; NID:9177974; PIDN:AAA6815.1; PID:9177975  
A:Note: this sequence represents composite of clones including clone ABGACHE from adult brain; should represent an authentic brain splice form  
R:Chajlant, V.; Derr, D.; Earles, B.; Schwell, E.; August, T.  
FEBS Lett. 247, 279-282, 1989  
A:Title: Purification and partial amino acid sequence analysis of human erythrocyte acetylcholinesterase.  
A:Reference number: S03959; MUID:89232136; PMID:2714437  
A:Accession: S03959  
A:Molecule type: protein  
A:Residues: 256-266, 'Y', 268-273; 306-308, 'X', 310-313, 'X', 315-316, 'D', 318-323, 'D', 325-326, 'Y', 532-551 <CH>  
A:Experimental source: erythrocytes  
A:Note: this form was a disulfide-linked homodimer  
C:Genetics:  
A:Gene: GDB:ACHB; YT  
A:Cross-references: GDB:118746; OMIM:100740  
A:Map position: 7q22-7q22  
C:Superfamily: cholinesterase; cholinesterase homology  
C:Keywords: alternative splicing; carboxylic ester hydrolase; glycoprotein; phosphatidylcholine; signal sequence #status predicted <SIG>  
F:63-569/Domain: cholinesterase homology <CH>

Query Match 54.3%; Score 1689; DB 2; Length 614;  
Best Local Similarity 52.8%; Pred. No. 2.2e-121; Indels 8; Gaps 5;  
Matches 307; Conservative 104; Mismatches 162;

1 ED-DIIATKNGKRGKGMNLTVPFGTVAFLGIPYAPPLGRLRFRKPKQSLTKMSDINWATK 59  
35 EDSELIVNTKSGKMTKRTIPVLSHISAFGLGFPAEPVGMRRPRRPPKPKWGSVWNAAT 94  
60 KYANSCCONIDQSPFGFGSEMMNPTDLSDDCLYNWIPAKPKKAT-VLIWYGGF 118  
95 TFGSVCQYVDTLYPFGFGSEMMNPTDLSDDCLYNWIPAKPKKAT-VLIWYGGF 154  
119 QGTSSLHYDQKFLARVERVIVSMNRYGALGFLALPGNPAAGMGLDQRLALQWV 178  
155 YGASLSDYDQKFLARVERVIVSMNRYGALGFLALPGNPAAGMGLDQRLALQWV 214  
179 QKNIIAFGNPKSVTLFGESAGAASVLSLSPGSHLFTTRAILQSGSFNAPAWATSLYE 238  
215 QENVAAFGDPRKTVTLFGESAGASVGMHLSFGSDLRRAILQSGSNCMAVSVAEGR 274  
239 ARNRTNLAKLTGCSRENETEIIKCLRNKPOEILINAEFVVPYGTPLSVNFGPTVDG 294  
275 ARRAATQALAVCCPRGTCGNDTELVACLRTPAQVLTVMHEWVLPQESVFRFSFV 334  
295 DGEFLDMDPILLELQFKKTOILVGNKDEGFWPLVYGA RGSKDNNSITRKEFOEGLKIF 354  
335 DGEFLDMDPILLELQFKKTOILVGNKDEGFWPLVYGA RGSKDNNSITRKEFOEGLKIF 394  
355 KIFPGVSEBGEKESILFHYTDWVDQRPENYREALGDVVDYVFCPALFTFKKFSWGN 414  
395 RGVGPVSDLAALAAVLTHTDMLHPDPRALRALSDVGDHVICPLMFVAKYTKFGYGLY 454  
415 NAEFYFHEHSSSLPMEWVGVIHGYEIEFVGLPLVKEILNTYAEBAALSRRIMHWATPAK 474  
455 RYAAVYFHEHSSSLPMEWVGVIHGYEIEFVGLPLVKEILNTYAEBAALSRRIMHWATPAK 514  
475 AKYGNPEON-NSTMPVFKSTQKTLTNTSTRIMTKLRAQOCRFWTSFPFKVLEMT 533  
515 AKTGDPNEPRDPYAPQWPTTAGAQVSDLRPLEVRKGLAQACAFNRFLPKLSAT 574  
534 GNIDAEAEWEMKAGFRHNNVMDKQNFNDYTSKESCVGL 574







Qy 530 LEMTGNIDEAEWKAQFHRM-NNYMADWKNQFNDY-----TSKESCVG 573  
Db 569 MAADVADGDPYLWVKQMDKQNEIYITDQWHEFYKRYQYRSDSETGCG 620

## RESULT 13

S66236  
acetylcholinesterase (EC 3.1.1.7) precursor - yellow fever mosquito  
C/Species: Aedes aegypti (yellow fever mosquito)  
C/Date: 14-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004  
C/Accession: S66236  
R/Author: N. Rocheleau, T. Mocolin, G. Lee, H.J. ffrench-Constant, R.  
FEMS Lett. 368, 461-465, 1995  
A/Title: Cloning, sequencing and functional expression of an acetylcholinesterase gene  
A/Reference number: S66236; MUID:55361924; PMID:7635199  
A/Accession: S66236  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-637 <ANT>  
A/Cross-references: UNIPROT:Q9TX11  
C/Superfamily: cholinesterase; cholinesterase homology  
C/Keywords: carboxylic ester hydrolase  
F;1-28/Domain: signal sequence #status predicted <SIG>  
F;29-637/Product: acetylcholinesterase #status predicted <MAT>  
F;57-594/Domain: cholinesterase homology <CHE>

Query Match 34.4%; Score 1070.5; DB 2; Length 637;  
Best Local Similarity 38.9%; Pred. No. 6e-74; Mismatches 207; Indels 53; Gaps 8;  
Matches 223; Conservative 90;

Qy 2 DDIIATKNGKVGKGMNLTGFGVTATFLGIPYAPQPLGRLEFKKQSLTKMSIDMNAKY 61  
Db 31 DRIVVQSSGPGRKRSIMVLGRVHNGVPFAKRPVDGRFRKRPVAPAEHMGVLDATRL 90  
Qy 62 ANSCCNIDSPFGFSGSEMNPNPTDLSDDLINWIPAP----- 101  
Db 91 PPSCIQREYEPFGFAGEEMWNPNTNVEDCLINWIPAKPVEDRFRKRPVAPAEHMGVLDATRL 150  
Qy 102 -----PKPKATVLIWYGGFQGTSSLHYDQGLKFLARVERIVVSNMRYVALGF 153  
Db 151 DDDFORHQSGKGLAMLVWYGGGFMSTLTDVYNEMLAAGNVIVASMQYKVGSGFG 210  
Qy 154 LALP---GNPEAPGNMGLPQOOLALQWOKIAAFGNGPKSVTLFGESAGAAVSILHLS 210  
Db 211 FYLAPYINDDDAFGNVGLMDALAIRWIKENAKAFSGDPDLITLFGESAGSSVSILHLS 270  
Qy 211 PGSHSLFTRAILQSGSFNAPMAVTSLYEARNRTLNAKLTGCS-----RENETELIKCLRN 266  
Db 271 PVRGSLRGLIGSTLNAIPMSHSAEKALSVAAALIDDCNCVTLTKDNPVYMNCMRN 330  
Qy 267 KDPQELLINAEFVVPYPTPLSVNFGPTVDDGLTMDLILLEGQFKTQILVANKDEG 326  
Db 331 VDAKTSIVQO--WNSYSGILGFPSPAPITDVFMTADMTMLREANLEGVLEILVGSNDEG 388  
Qy 327 TWPLFVNG-APGFSKDNNSIITRKEFOGLKIFPPVSEFGKESILFHYTMVDDQRENY 385  
Db 389 TYFLVDFITYFEKDAATSLPRDKFLIEMWTIFSKASBPERRAIIIFQYTGESANDQYON 448  
Qy 386 REALGVVGVNFIKPALEFTKFSSEWGNNAFFYYFHEHRSKLPWPMGMVMSYELEFV 445  
Db 449 QQQQGRSGVGHFICPTNEFALGLAERGASVYVYFTHRTSTSLMGEMGVLDHDEVYI 508  
Qy 446 FGLPLERDNYTKAEELLSRSIVKMANPAKYGNPNETONNSTSWPVFKSTEQKIYTLANT 505  
Db 509 FGQPMNVSMQYRQREPLSRMVLVSSEFARSQNP--ALEGHEMPVYTKENPIYFLENA 565  
Qy 506 ESTRIWTKLRQO-----CRFWTSPPPKV 529  
Db 566 EGE---DDLNGEKYGRGPMTATACAFMDFLPRLL 595

RESULT 14

A25363  
acetylcholinesterase (EC 3.1.1.7) precursor - fruit fly (Drosophila melanogaster)  
C/Species: Drosophila melanogaster  
C/Date: 16-Aug-1988 #sequence\_revision 31-Dec-1988 #text\_change 09-Jul-2004  
C/Accession: A25363; A33469  
R/Hall, L.M.C.; Splerer, P.  
EMBO J. 5, 2949-2954, 1986  
A/Title: The Ace locus of Drosophila melanogaster: structural gene for acetylcholinesterase  
A/Reference number: A25363; MUID:87080281; PMID:3024971  
A/Accession: A25363  
A/Molecule type: mRNA  
A/Residues: 1-746 <HAL>  
A/Cross-references: UNIPROT:P07140  
A/Note: the authors translated the codon TGG for residue 18 as Cys and AGA for residue 27.  
R/Fournier, D.; Karch, F.; Bride, J.M.; Hall, L.M.C.; Berge, J.B.; Splerer, P.  
J. Mol. Biol. 210, 15-22, 1989  
A/Title: Drosophila melanogaster acetylcholinesterase gene structure, evolution and mutation  
A/Reference number: A33469; MUID:9064544; PMID:2511327  
A/Accession: A33469  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 98-746 <FOU>  
A/Cross-references: GB:X17572  
C/Genetics:  
A/Gene: FlyBase: Ace  
A/Cross-references: FlyBase: FBgn0000024  
C/Superfamily: cholinesterase; cholinesterase homology  
C/Keywords: carboxylic ester hydrolase  
F;164-704/Domain: cholinesterase homology <CHE>

Query Match 33.6%; Score 1044; DB 2; Length 746;  
Best Local Similarity 37.9%; Pred. No. 8.2e-72;  
Matches 223; Conservative 100; Mismatches 204; Indels 60; Gaps 12;

Qy 2 DDIIATKNGKVGKGMNLTGFGVTATFLGIPYAPQPLGRLEFKKQSLTKMSIDMNAKY 61  
Db 138 DRIVVQSSGPGRKRSIMVLGRVHNGVPFAKRPVEDRFRKRPVAPAEHMGVLDATRL 197  
Qy 62 ANSCCNIDSPFGFSGSEMNPNPTDLSDDLINWIPAP----- 102  
Db 198 SATVOERIEYFPFGFSGEELMNPNTNVEDCLINWIPAKPVEDRFRKRPVAPAEHMGVLDATRL 257  
Qy 103 -----KPKATVLIWYGGFQGTSSLHYDQGLKFLARVERIVVSNMRYVALGF 148  
Db 258 ADTDHILHNGNPQNTNGLPLIWIYGGFMSTATLDIYNADIMAAVGNVIVASMQYKVGSGFG 317  
Qy 149 GAGFLAL-PGNP---EAPGNMGLPQOOLALQWOKIAAFGNGPKSVTLFGESAGAA 202  
Db 318 GARGFLALPEMSEFAEAPGNVGLMDALAIRWIKENAKAFSGDPDLITLFGESAGSSVSILHLS 377  
Qy 203 SVSILHLSPGSHSLFTRAILQSGSFNAPMAVTSLYEARNRTLNAKLTGCS-----REN 256  
Db 378 SVNAQLMSFVTRGLVKGGMQSGTMNAPMSHMTSEKAVR--IKALINDCNASMLKTN 435  
Qy 257 ETEIILKLNKDKQOEILLINAEFVVPYPTPLSVNFGPTVDDGLTMDLILLEGQFKTQ 316  
Db 436 PAVTMGMSVDAKTSIVQO--WNSYSGILGFPSPAPITDVFMTADMTMLREANLEGVLEILVGSNDEG 493  
Qy 317 ILVGVNKGSTWPLVYG-APGFSKDNNSIITRKEFOGLKIFPPVSEFGKESILFHYTMVDDQRENY 375  
Db 494 ILMGNVNDEGTYFLALVDIFDIPDKDATALPRDKYLEIMNNIIGKATQARERAIIIFQYTGESANDQYON 553  
Qy 376 WVDQRENYREALGVVGVNFIKPALEFTKFSSEWGNNAFFYYFHEHRSKLPWPMGMVMSYELEFV 435  
Db 554 WEGNPGYON-QQQIGRAVGDHFTCTNEAQAOLARASVHYVYFTHRTSTSLMGEMGVLDHDEVYI 612  
Qy 436 VMHGEIEFVFGPLERDNYTKAEELLSRSIVKMANPAKYGNPNETONNSTSWPVFKS 495  
Db 613 VHGDEIEYFQGPLNNSIYQRYVEREIGKRMASVHIEPAKIGNPQO---DGEWENFISK 669  
Qy 496 TEQKIYTLANTESTRIWTKLR---AQCRFWTSPPPKV 537  
Db 670 EDPVYIYFSTDCK--IEKLARGPLAARCSFWDYLPKRVSWAGTCD 713







A;Residues: 1-602 <GRA>  
 A;Cross-references: UNIPROT:O61372; EMBL:AF025379; NID:G5091493; PIDN:AA014017.1; PID:G3  
 A;Experimental source: strain N2  
 C;Genetics:  
 A;Gene: ace-4  
 C;Superfamily: cholinesterase; cholinesterase homology  
 C;Keywords: carboxylic ester hydrolase

Query Match 32.6%; Score 1012.5; DB 2; Length 602;  
 Best Local Similarity 38.1%; Pred. No. 1.5e-69;  
 Matches 212; Conservative 92; Mismatches 195; Indels 57; Gaps 12;

```

Qy 4 IIAATKNGKVRGMNLTVEGTVTAFLGIPYAPQPLGRLEPKKQPSLTWSDIWNATKYAN 63
  :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 27 VVLETKGDIKSTGEFFLSKKIRTFPGVPAPPAVEDPFRPKPRKKQWRLYATKPAN 86
  :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 64 SCCONIDQSPFGPFGSEKMNPTDSEDCLYLNWTPAPKPKATVLIWYGGSPQGT 123
  :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 87 ACFTGRNNTYTSFWSSEKMNANTQISDCLYLNWTPA-DAYNLTWVWFGGSPYSGSP 145
  :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 124 SLHYDGKFLARVRYVSMNRYVAGALGFLALPGNPAAGMGLFPQQLALQWVOKNIA 183
  :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 146 SLSTYDGKALSTQNVVNVNNTYLGPPGFLYL-GHPDAPGNMGLDQQLALHWVONIV 204
  :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 184 AFGNPKSVTLFGESAGAAVSILHLSPGSHSLFTRAILQSGSFNAPWATSLYEARNR 243
  :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 205 SFGNPKSVAVFGGAGAAIVAHILAPGSRGLFKNALIQGSLNWTWAINSPRAKKS 264
  :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 244 LNLAKLTGSRNENETIICKLRNKPQELLNENAFVVPYGTPLSVNGPVL----- 294
  :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 265 EKLELVGCKNTYVDTSMACLRIVSPQSLIS-----TWNISLTYLEFPFVIVSRDKHF 319
  :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 295 -----DGFPLTMDPILLELQPKQIILVGNVDEGTWLVYAGAPG-PSKDNNS 343
  :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 320 GHLDHAHALBEGDNRD-----NLKIMGNKDEGNWNTYOLDFQFDKADPP 366
  :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 344 IITRKEFQELKIFPGVSEFGKESILFHYTD--WVDQREPN-YREALGVVDGYNTIC 400
  :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 367 ELNRTERDPLIDRFSTQPDILRSAAKIYSDPCTDHGRKTRFYAQQMNVIGDYFSC 426
  :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 401 PALEFTKPF-----SEGNNAFFYYFEHRSSKLPPEPMGMHGYEIEFVGLP 449
  :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 427 DSLMLAQFQPSIPRVKSSPQRKPKGVVYHFTOSSSANPWPKWGTGMHGYEIEYVGI 486
  :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 450 LERDNTKAEELISRIYKWMANFAKYGNPN-ETONNSTSWPWF-KSTEQKYLNTMES 507
  :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 487 LYSKNTKRRRQIFSRKIMQFMAFAKNGTPKLRVLKNSHSEPMFNEONHRYRMQLRSGS 546
  :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 508 TRIMTKLRAQ-QCRFW 522
  :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 547 NIRPIKPKQVQCQFW 562
  :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

```

RESULT 18  
 T37255  
 acetylcholinesterase (BC 3.1.1.7) 2 - Caenorhabditis elegans  
 C;Species: Caenorhabditis elegans  
 C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
 C;Accession: T37255  
 R;Grauho, M.; Culetto, E.; Combes, D.; Fedon, Y.; Toulant, J.P.; Arpagaus, M.  
 FEBS Lett. 424, 279-284, 1998  
 A;Title: Existence of four acetylcholinesterase genes in the nematodes Caenorhabditis el  
 A;Reference number: Z21648; MUID:99199570; PMID:9539167  
 A;Accession: T37255  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-629 <GRA>  
 A;Cross-references: UNIPROT:O61371; EMBL:AF025378; NID:G5148937; PIDN:AA014016.2; PID:G5  
 A;Experimental source: strain N2  
 C;Genetics:  
 A;Gene: ace-2  
 A;Map position: 1  
 C;Superfamily: cholinesterase; cholinesterase homology

C;Keywords: carboxylic ester hydrolase

Query Match 30.5%; Score 948; DB 2; Length 629;  
 Best Local Similarity 38.4%; Pred. No. 1.5e-64;  
 Matches 221; Conservative 92; Mismatches 193; Indels 70; Gaps 20;

```

Qy 3 DIIATKNGKVRGMNLTVEGTVTAFLGIPYAPQPLGRLEPKKQPSLTWSDIWNATKYA 62
  :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 38 DHVHTFPLGIRIGVGQFPDAKVASAFGLGVYAKPPIGSRFFKAAEMIDRSGELEATTLA 97
  :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 63 NSCCONIDQSPFGPFGSEKMNPTDSEDCLYLNWTPAPKPKATVLIWYGGSPQGT 122
  :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 98 KCTYLTIDSAFPQPGAEEMNPPGALSEDCLYLNWTPA--PEDHGSVMWVYGGSPFSGT 155
  :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 123 SLHYDGKFLARVRYVSMNRYVAGALGFLALPGNPAAGMGLFPQQLALQWVOKNIA 182
  :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 156 PSLDIVSGSFAPAKEHTIVNVNRYLGPFFLYLFGDSDPIQGMNGLDQQLALRWVHNTI 215
  :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 183 AAFGNPKSVTLFGESAGAAVSILHLSPGSHSLFTRAILQSGSFNAPWATSLYEARNR 242
  :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 216 GAFGDRSRVTLFGESAGASITTAHLFAPNSHYFRNIIAKSGSIINSWASATPPTWLDL 275
  :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 243 TLNLAKLTGSRNENETIICKLRNKPQELLNENAFVVPYGTPLSVNGPVL----- 299
  :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 276 SFRLAKVNCSSPDMAIVCLRSV--PAHLVQADNITSGDIPBMTFAVVPSSDANPF 334
  :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 300 TDMEDILLEG--QFKK-TQILVGNKDEGTWLVY--GAP--GFS-----KDNNS 343
  :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 335 --QGVVQKLANQPKDVNIIIFGSYKDEBTWLPYMSLPKXGFANHTISADPNRRA 392
  :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 344 IITRKEFQELKIFPGVSEFGKESILFHY-----TWVDQREPNYREALGVVDGY 395
  :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 393 LITRDHYEBSRAFMFPYFA--GSKLVLANFMSYEHVSTNVPEER---YRDGVARPLGD 447
  :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 396 YNFIQPALEFTKPFSE--WNNNAFFYYFEHRSSKLPPEPMGMHGYEIEFVGLP 453
  :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 448 LFTFCSLIDPADLISDIFG--NVMYFFYTRSSANPWPKWGTGMHGYEIEYVQFWRP 506
  :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 454 DNYTKA-----EELISRIYKWMANFAKYGNPNETONNSTSWPWF-KSTEQKYLNTMES 508
  :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 507 HLYDQTLDEBKLSLIMQIMANFANTG-----RDSWPQYNTKERAIEIG-ETTL 559
  :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 509 ----RIMTKLRAOQCRFWTSPFPKVLMTGNIDAE 540
  :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 560 QGKRRIISDVHGFCRW-----IDEAK 581
  :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

```

RESULT 19  
 T27009  
 hypothetical protein Y48B6A.8 - Caenorhabditis elegans  
 C;Species: Caenorhabditis elegans  
 C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
 C;Accession: T27009  
 R;Mail, M.  
 submitted to the EMBL Data Library, September 1999  
 A;Reference number: Z20297  
 A;Accession: T27009  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 1-584 <WTL>  
 A;Cross-references: UNIPROT:Q09295; EMBL:AL110490; PIDN:CA054453.1; CESP:Y48B6A.8  
 A;Experimental source: clone Y48B6A  
 C;Genetics:  
 A;Gene: CESP.Y48B6A.8  
 A;Intons: 24/3; 58/2; 132/2; 241/2; 461/2; 514/2  
 C;Superfamily: cholinesterase; cholinesterase homology

Query Match 30.1%; Score 937; DB 2; Length 584;  
 Best Local Similarity 38.4%; Pred. No. 9.1e-64;  
 Matches 208; Conservative 93; Mismatches 205; Indels 36; Gaps 16;

```

Qy 6 IATKNGKVRGMNLTVEGTVTAFLGIPYAPQPLGRLEPKKQPSLTWSDIWNATKYANSC 65
  :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

```

```

Db      34 VQTKLGTGRGTSBDHGNKRVRSFLGVPAEPPIINEHRFKKPTPARPWNGTISANTLSPAC 93
Qy      66 CQNIIDQSPFGHSEMNPNPTDISEDCLYLNMWIPARKKNATVLIWYGGGFGQTGSSL 125
Db      94 FQGRDSYDPTFWGSEMNANTPVSEDCLYNIMAPA-DAYNLTVLWLFGGGFWYGSPL 152
Qy      126 HYYDGKFLAVERIVVSNMRYVAGLGPLALPGNPEAPNGMLFDQOLALQWYQKNIAP 185
Db      153 LLYDGKELATRGNVIVNINRYVPGYLFL-DHEDVPGNMGLDQOLALYIRDHIFSF 211
Qy      186 GGNPKSVTLFGESAGASVSLHLSFGSHLFTRALILOGSFNAPWAVTSLEYARNRTLN 245
Db      212 GGNPARISLVGSAGASIVAHILAPASKGLFQNGILOGSLDNKMSMDSPKRAQKOSTA 271
Qy      246 LAKLTGCSRENETEIKLRNKPQELLNBAFVVPYG---TPLSV---NFGPTVGD 297
Db      272 LADLVGCNQTITDQACLRN-TPAQLIDINWVGNLFEPFPAIVSKQNFKHLIDG- 329
Qy      298 FLTMDPILLELGQFK-KTOILVGVNDEGTWFLVYGAFGFSKDNNSI---ITRKEFOG 353
Db      330 -----FILREGYSTDVNLMEGINHDEGNFWNIYMLAKFF-DKQSVKGLDRDEFEHC 382
Qy      354 LKIFPGEVSEFGKESILFHYTD--WVDQRPEN-YREALGVGDYVNFICPALFETKFS 410
Db      383 VDTAFVQPELVRTAKVYVSDPKCTDPKKKTDFYEQVQWQVGDYFFCTDSIFAHNYP 442
Qy      411 EW-GN--NAFFYFEHRSKLPPEWGMVHGIEIEFVGLPLERRD-NYTKAEILSR 466
Db      443 KMAQNSVFFVYFDQSSANPMPKWTGVHGYIEVFGVPLHNTTAGTYKEEMDVSEK 502
Qy      467 IYKRNAPKAGYGNPTQ-----NSTSWPVKSTEO-KYLLTNESTETIMTKLRAOQR 520
Db      503 VIDFWTTFANTGVPSLRKRAVGTQKIKWDRYDGDHTMTMMNITGSPFMIOBKVCECD 562
Qy      521 FW 522
Db      563 LW 564

```

## RESULT 20

```

T42399
acetylcholinesterase (EC 3.1.1.7) - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C/Accession: T42399
R/Grauso, M.; Culetto, E.; Fedon, Y.; Combes, D.; Toutant, J.P.; Arpagaus, M.
submitted to the EMBL Data Library, June 1999
A/Reference number: Z22157
A/Accession: T42399
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-607 <GRA>
A/Cross-references: UNIPROT:O61459; EMBL:AF039650; PDB:AA014022.2
A/Map position: 2
A/Map position: 2
C/Superfamily: cholinesterase; cholinesterase homology
C/Keywords: carboxylic ester hydrolase

```

```

Query Match      29.9%; Score 930; DB 2; Length 607;
Best Local Similarity 38.2%; Pred. No. 3.3e-63;
Matches 207; Conservative 93; Mismatches 206; Indels 36; Gaps 16;

Qy      6 IATKNGKRGKMLTVFGGTVTAFLGIPYAQPLGRLPKPKQSLTKMSDINATKYANSC 65
Db      34 VQTKLGTGRGTSBDHGNKRVRSFLGVPAEPPIINEHRFKKPTPARPWNGTISANTLSPAC 93
Qy      66 CONIDQSPFGHSEMNPNPTDISEDCLYLNMWIPARKKNATVLIWYGGGFGQTGSSL 125
Db      94 FQGRDSYDPTFWGSEMNANTPVSEDCLYNIMAPA-DAYNLTVLWLFGGGFWYGSPL 152
Qy      126 HYYDGKFLAVERIVVSNMRYVAGLGPLALPGNPEAPNGMLFDQOLALQWYQKNIAP 185

```

```

Db      153 LLYDGKELATRGNVIVNINRYVPGYLFL-DOEDVPGNMGLDQOLALYIRDHIFSF 211
Qy      186 GGNPKSVTLFGESAGASVSLHLSFGSHLFTRALILOGSFNAPWAVTSLEYARNRTLN 245
Db      212 GGNPARISLVGSAGASIVAHILAPASKGLFQNGILOGSLDNKMSMDSPKRAQKOSTA 271
Qy      246 LAKLTGCSRENETEIKLRNKPQELLNBAFVVPYG---TPLSV---NFGPTVGD 297
Db      272 LADLVGCNQTITDQACLRN-TPAQLIDINWVGNLFEPFPAIVSKQNFKHLIDG- 329
Qy      298 FLTMDPILLELGQFK-KTOILVGVNDEGTWFLVYGAFGFSKDNNSI---ITRKEFOG 353
Db      330 -----FILREGYSTDVNLMEGINHDEGNFWNIYMLAKFF-DKQSVKGLDRDEFEHC 382
Qy      354 LKIFPGEVSEFGKESILFHYTD--WVDQRPEN-YREALGVGDYVNFICPALFETKFS 410
Db      383 VDTAFVQPELVRTAKVYVSDPKCTDPKKKTDFYEQVQWQVGDYFFCTDSIFAHNYP 442
Qy      411 EW-GN--NAFFYFEHRSKLPPEWGMVHGIEIEFVGLPLERRD-NYTKAEILSR 466
Db      443 KMAQNSVFFVYFDQSSANPMPKWTGVHGYIEVFGVPLHNTTAGTYKEEMDVSEK 502
Qy      467 IYKRNAPKAGYGNPTQ-----NSTSWPVKSTEO-KYLLTNESTETIMTKLRAOQR 520
Db      503 VIDFWTTFANTGVPSLRKRAVGTQKIKWDRYDGDHTMTMMNITGSPFMIOBKVCECD 562
Qy      521 FW 522
Db      563 LW 564

```

## RESULT 21

```

T33842
hypothetical protein Y44E3A.2 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C/Accession: T33842
R/Moesener, J.; Graves, T.; Keppler, D.
submitted to the EMBL Data Library, November 1998
A/Description: The sequence of C. elegans cosmid Y44E3A.
A/Reference number: Z21422
A/Accession: T33842
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-532 <MOE>
A/Cross-references: UNIPROT:O61371; EMBL:AF106589; PDB:AA078228.1; GSPDB:GN00019; CESP:
A/Experimental source: strain Bristol N2; clone Y44E3A
A/Genetic:
A/Map position: 1
A/Map position: 1
A/Intons: 16/3; 84/3; 143/2; 219/3; 298/3; 440/2
C/Superfamily: cholinesterase; cholinesterase homology

```

```

Query Match      28.7%; Score 893; DB 2; Length 532;
Best Local Similarity 40.8%; Pred. No. 1.9e-60;
Matches 201; Conservative 79; Mismatches 169; Indels 44; Gaps 16;

Qy      19 TVFGGTVTAFLGIPYAQPLGRLPKPKQSLTKMSDINATKYANSCQNIIDQSPFGFG 78
Db      17 TFGQAKYSAPFLGIPYAKPFGSRFRKAEIMDNSELEAKTLCYLTIDSAFQFPG 76
Qy      79 SEMNPNPTDISEDCLYLNMWIPARKKNATVLIWYGGGFGQTGSSLHYYDGKFLAVER 138
Db      77 AEMNPNPGALISEDCIMNINIV--PEHDHDSVWVWYIGGGFSGTSPSLDYSGVFAKEH 134
Qy      139 VIVSNMRYVAGLGPLALPGNPEAPNGMLFDQOLALQWYQKNIAPFGNPKSVTLFGES 198
Db      135 TIVNVMYVRIGPFGFLVFGDSDPIQNGMGLMDQOLLRWHENIIGAFGGDRSVTLFGES 194
Qy      199 AGAASVSLHLSFGSHLFTRALILOGSFNAPWAVTSLEYARNRTLNALKTGCSRENET 258
Db      195 AGSASTTAHLFAPNSHKYFNINIIAKSGSIINSWASATPPTMLDLRLAKKNCSSPDMN 254

```

QY 259 EIIKCLANKPOEILLNEAFV--PYGTPLSVNFGP-TVDDPFLTMDILLLEG--QFK 313  
 DB 255 AIVKCLASV--PAHVOEADNIGSDIGPMTFAVVPVSSDANF--QGDVQKLANQKFK 311  
 QY 314 K-TQILVGVNDCEGTWLVY--GAP--GFS-----KNNSTITRKEQOGLKIFP 359  
 DB 312 KDVAIIIFGSVYDEBTYWLPHYMSLPKYGFAFNHTISAEDPNRLITRDHYESMRAFP 371  
 QY 360 GVSEFGKESILFHY-----TMDVDDORPENYREALGVGDYVFCPALBFTKKESE 411  
 DB 372 YFA--GSKLVANAMNSYEHSTSNVPER--YRDGARFLGDLFFTCSLIDPADLISD 426  
 QY 412 --WGNNAFFYYFEHRSSKLPMEWGVNHYEIEFVGLPERDNTYKA---EELLIS 465  
 DB 427 NIFG-NVYMYFTYRSSANPMPKMWGVNHYEIEVAFQPYWRPHLYDQTHLEDEKRLSS 485  
 QY 466 SIYKMANPAKY 478  
 DB 486 IIMQIMANFANTG 498

RESULT 22

A34329  
 60K esterase (EC 3.1.1.-) isoform 2 - rabbit  
 C/Species: Oryctolagus cuniculus (domestic rabbit)  
 C/Date: 22-Jun-1990 #sequence\_revision 22-Jun-1990 #text\_change 09-Jul-2004  
 C/Accession: A34329  
 R/Octol. J.  
 J. Biol. Chem. 264, 12533-12545, 1989  
 A/Title: Isolation, properties, and the complete amino acid sequence of a second form of  
 A/Reference number: A34329; PMID:89308686; PMID:2745458  
 A/Accession: A34329  
 A/Status: preliminary  
 A/Molecule type: protein  
 A/Residues: 1-532 <OZO>  
 C/Cross-references: UNIPROT:P14943  
 C/Superfamily: cholinesterase; cholinesterase homology  
 C/Keywords: carboxylic ester hydrolase  
 F/32-517/Domain: cholinesterase homology <CHE>  
 F/201,430/Active site: Ser, His #status predicted

Query Match 24.2%; Score 754; DB 2; Length 532;  
 Best Local Similarity 36.1%; Pred. No. 8.5e-50;  
 Matches 199; Conservative 90; Mismatches 202; Indels 60; Gaps 22;  
 QY 8 TKNGKXKGNMLTVRG--GTVAFIGIPYAOPIGLRPPKQSLTKXSDINNAKTVNSC 65  
 DB 10 THTGQVRGSLVHVETDAGVHTFLGIPAKPLGLRPAPEPAEAMSGVADGTSLPAMC 69  
 QY 66 CONT---DQSPFGHSEMMNPTDLSBDCLYLWVWIP--APKPKNATVLWYGGGFQT 120  
 DB 70 LQNLAIMDQVLLHFP--PSIPMSBDCLYLWVWIP--APKPKNATVLWYGGGFQT 126  
 QY 121 GTSSLHVYDGFKLARVERVIVSNMRYGALGFALPGNPAQNMGLFDQQLALQWVQK 180  
 DB 127 GMAISM--YDGSALAFEDVVVVTIQRRLGVLFPS--TGDDQATGNHGYLDQVALRWQK 183  
 QY 181 NIAAFGNPKSVTLFGESAGAAVSLSLHSGSLSLFRALQSGSFAPAVATSLYAR 240  
 DB 184 NIAAFGNPKSVTLFGESAGAAVSLSLHSGSLSLFRALQSGSFAPAVATSLYAR 243  
 QY 241 NRTNLAKLNGCSENEETIKKCRNKDPOEL-LINEAFVVPYGPPLSVNNGPVDGFL 299  
 DB 244 STV--VANLSRCGVDSSTLVRCLRAKSEEMLITVFMILPG-----VVDGVFL 292  
 QY 300 TMDPILLELQGFKKTOILVGVNDCEGTW---FLVYGAPSPKDNNSITRKEFORGLK 355  
 DB 293 PRHREELALADFPVPSIIGINDXEWIIPKLLAIDPBERDQGM--REIMHQATK 350  
 QY 356 --TFPGVSEKGSILFHTYDWDQDRENYREALGVGDYVFCPALBFTKKESE 413  
 DB 351 QLMPLPALGDL---LMDEYGSNED--PKILMAQOFEMADAMFVMPALR--VAHLORSH 403

QY 414 NNAFFYYFEHRSS--KLPMPEWGVNHYEIEFV-----GLPERDNTYKAELLIS 464  
 DB 404 APYFYEFQRRSPPTKOLRPPHVRADHGVFVFRSHLFGSKVPL-----TEEBELLIS 457  
 QY 465 RSIYKMANPAKYNPETQNNSTWPFVSKTECKYTLTNTESRINTKLRAOOCRRWTS 524  
 DB 458 RRVKRYANPARNNPN--GEGLAHPLF-DLDQRYQLNMQPA-VQALKAARLQFWTH 513  
 QY 525 FFP-KVLEMTG 534  
 DB 514 TLPRVQVELNG 524

RESULT 23

G39768  
 cholinesterase (EC 3.1.1.8) - rhesus macaque (fragment)  
 C/Species: Macaca mulatta (rhesus macaque)  
 C/Date: 14-Feb-1992 #sequence\_revision 14-Feb-1992 #text\_change 09-Jul-2004  
 C/Accession: G39768  
 R/Arpagaus, M.; Chatonnet, A.; Masson, P.; Newton, M.; Vaughan, T.A.; Bartels, C.F.; Nogi  
 J. Biol. Chem. 266, 6966-6974, 1991  
 A/Title: Use of the polymerase chain reaction for homology probing of butyrylcholinesterase  
 A/Reference number: A39768; PMID:91201348; PMID:2016308  
 A/Accession: G39768  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-141 <ARP>  
 A/Cross-references: UNIPROT:P32751; GB:M62777; NID:G342078; PIDN:AAA36836.1; PID:G342079  
 C/Superfamily: cholinesterase; cholinesterase homology  
 C/Keywords: carboxylic ester hydrolase; glycoprotein  
 F/1-141/Domain: cholinesterase homology (fragment) <CHE>

Query Match 24.2%; Score 753; DB 2; Length 141;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-50;  
 Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 68 NIDQSPFGHSEMMNPTDLSBDCLYLWVWIPAPKPKNATVLWYGGGFQGTSSLHV 127  
 DB 1 NIDQSPFGHSEMMNPTDLSBDCLYLWVWIPAPKPKNATVLWYGGGFQGTSSLHV 60  
 QY 128 YDGFKLARVERVIVSNMRYGALGFALPGNPAQNMGLFDQQLALQWVQKIAAFPG 187  
 DB 61 YDGFKLARVERVIVSNMRYGALGFALPGNPAQNMGLFDQQLALQWVQKIAAFPG 120  
 QY 188 NPKSVTLFGESAGAAVSLSLH 208  
 DB 121 NPKSVTLFGESAGAAVSLSLH 141

RESULT 24

A57701  
 sterol esterase (EC 3.1.1.13) precursor - mouse  
 N/Alternate names: bile salt-stimulated lipase; carboxyl ester lipase; cholesterol esterase  
 C/Species: Mus musculus (house mouse)  
 C/Date: 23-Feb-1996 #sequence\_revision 23-Feb-1996 #text\_change 09-Jul-2004  
 C/Accession: A57701; J04384  
 R/Lidmer, A.S.; Kamius, M.; Lundberg, L.; Bjursell, G.; Nilsson, J.  
 Genomics 29, 115-122, 1995  
 A/Title: Molecular cloning and characterization of the mouse carboxyl ester lipase gene  
 A/Reference number: A57701; PMID:96079098; PMID:8530060  
 A/Accession: A57701  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-599 <LID>  
 A/Cross-references: UNIPROT:Q64285; GB:U37386; NID:G1049321; PIDN:AA52279.1; PID:G1049321  
 R/Mackay, K.; Lam, R.M.  
 Gene 165, 255-259, 1995  
 A/Title: Characterization of the mouse pancreatic/mammary gland cholesterol esterase-enc  
 A/Reference number: J04384; PMID:96096531; PMID:8522186  
 A/Accession: J04384  
 A/Molecule type: mRNA  
 A/Residues: 1-599 <MAC>  
 A/Cross-references: GB:U33169; NID:G1046362; PIDN:AAA92088.1; PID:G1046363



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## OM protein - protein search, using sw model

Run on: January 6, 2005, 09:41:48 ; Search time 160 Seconds  
(without alignments)  
1286.941 Million cell updates/sec

Title: US-09-748-739a-2\_COPY\_29\_602  
Perfect score: 3110  
Sequence: 1 EDIIIIATKNGKVRGMNLIV.....MDWKQFNQDYTSKSKSCVGL 574

Scoring table: BL0SUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729239 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 100 summaries

## Database :

1: Geneseq\_23Sep04:\*\n2: geneseqp1980s:\*\n3: geneseqp1990s:\*\n4: geneseqp2000s:\*\n5: geneseqp2002s:\*\n6: geneseqp2003as:\*\n7: geneseqp2003bs:\*\n8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3110	100.0	574	7	ABW00722 Human but
2	3110	100.0	602	5	AAO18897 Human but
3	3107	99.9	574	8	ADRO1039 Human but
4	3103	99.8	574	8	ADRO1047 Human but
5	3102	99.7	574	8	ADRO1051 Human but
6	3102	99.7	574	8	ADRO1035 Human but
7	3101	99.7	574	8	ADRO1041 Human but
8	3100	99.7	574	8	ADRO1037 Human but
9	3099	99.6	574	8	AAO18944 Human but
10	3098	99.6	574	8	ADRO1049 Human but
11	3096	99.5	574	5	AAE25235 Human but
12	3096	99.5	574	5	AAO18982 Human but
13	3096	99.5	574	5	AAO18988 Human but
14	3096	99.5	574	6	ABR62391 Human but
15	3096	99.5	574	7	ABW00695 Human but
16	3096	99.5	574	8	ADP44639 Human but
17	3096	99.5	574	8	ADRO1077 Human but
18	3096	99.5	602	3	AAV59235 Human but
19	3096	99.5	602	3	AAV49471 Human but
20	3096	99.5	602	3	AAV49473 Human but
21	3096	99.5	602	6	ABR62392 Human but
22	3096	99.5	602	8	ADP90908 Human but
23	3095	99.5	574	8	ADRO1045 Human but
24	3093	99.5	574	8	ADRO1059 Human but
25	3093	99.5	574	8	ADRO1075 Human but

26	3092	99.4	574	5	AAO18977 Human but
27	3092	99.4	574	7	ABW00723 Human but
28	3092	99.4	574	8	ADRO1080 Human but
29	3092	99.4	602	3	AAV44574 Human but
30	3091	99.4	574	5	AAO18979 Human but
31	3091	99.4	574	5	AAO18980 Human but
32	3091	99.4	602	3	AAV49483 Human but
33	3090	99.4	574	5	AAO18983 Human but
34	3090	99.4	574	5	AAO18945 Human but
35	3090	99.4	574	8	ADP44833 Human but
36	3090	99.4	574	8	ADRO1073 Human but
37	3090	99.4	602	2	AAV37442 Full-length
38	3089	99.3	574	5	AAO18981 Human but
39	3089	99.3	574	5	AAO18940 Human but
40	3089	99.3	574	8	ADRO1079 Human but
41	3089	99.3	574	8	ADRO1078 Human but
42	3089	99.3	602	3	AAV49474 Human but
43	3089	99.3	602	3	AAV49473 Human but
44	3089	99.3	602	3	AAV49475 Human but
45	3088	99.3	574	7	ABW00724 Human but
46	3088	99.3	574	8	ABW00725 Human but
47	3088	99.3	574	8	ADP44738 Human but
48	3088	99.3	574	8	ADRO1055 Human but
49	3088	99.3	574	8	ADRO1061 Human but
50	3088	99.3	574	8	ADRO1065 Human but
51	3088	99.3	574	8	ADRO1071 Human but
52	3088	99.3	574	8	ADRO1069 Human but
53	3088	99.3	602	3	AAV49472 Human but
54	3088	99.3	602	3	AAV49476 Human but
55	3087	99.3	574	5	AAO18978 Human but
56	3087	99.3	574	8	ADRO1063 Human but
57	3087	99.3	574	8	ADRO1043 Human but
58	3087	99.3	602	3	AAV49477 Human but
59	3086	99.2	574	5	AAO18942 Human but
60	3086	99.2	574	5	AAO18941 Human but
61	3086	99.2	574	8	ADP44765 Human but
62	3086	99.2	574	8	ADP44821 Human but
63	3086	99.2	574	8	ADRO1057 Human but
64	3086	99.2	574	8	ADRO1067 Human but
65	3085	99.2	574	5	AAO18899 Human but
66	3085	99.2	574	5	AAO18943 Human but
67	3085	99.2	574	5	AAO18901 Human but
68	3085	99.2	574	5	AAO18902 Human but
69	3085	99.2	574	8	ADP44800 Human but
70	3085	99.2	574	8	ADP44771 Human but
71	3085	99.2	602	3	AAV49484 Human but
72	3085	99.2	602	3	AAV49478 Human but
73	3084	99.2	574	5	AAO18976 Human but
74	3084	99.2	574	8	ADP44776 Human but
75	3084	99.2	574	8	ADP44810 Human but
76	3084	99.2	574	8	ADP44758 Human but
77	3084	99.2	574	8	ADP44780 Human but
78	3084	99.2	574	8	ADP44806 Human but
79	3084	99.2	574	8	ADRO1053 Human but
80	3084	99.2	602	3	AAV49486 Human but
81	3084	99.2	602	3	AAV49485 Human but
82	3084	99.2	602	3	AAV49488 Human but
83	3083	99.1	574	8	ADP44762 Human but
84	3083	99.1	574	8	ADP44769 Human but
85	3083	99.1	574	8	ADP44812 Human but
86	3083	99.1	574	8	ADP44770 Human but
87	3083	99.1	574	8	ADP44755 Human but
88	3083	99.1	574	8	ADP44772 Human but
89	3083	99.1	574	8	ADP44797 Human but
90	3083	99.1	574	8	ADP44739 Human but
91	3083	99.1	574	8	ADP44744 Human but
92	3083	99.1	602	3	AAV49478 Human but
93	3083	99.1	602	3	AAV49487 Human but
94	3082	99.1	574	5	AAO18960 Human but
95	3082	99.1	574	5	AAO18971 Human but
96	3082	99.1	574	5	AAO18933 Human but
97	3082	99.1	574	5	AAO18935 Human but
98	3082	99.1	574	8	ADP44756 Human but

99 3082 99.1 574 8 ADP44757 Adp44757 Human but  
100 3082 99.1 574 8 ADP44764 Adp44764 Human but

## ALIGNMENTS

## RESULT 1

ABW00722 standard; protein; 574 AA.

ABW00722;

15-JAN-2004 (first entry)

Human butyrylcholinesterase variant protein (A328W).

Human; butyrylcholinesterase; enzyme; mutant; mutein; variant.

XX Homo sapiens.

OS Synthetic.

Key Location/Qualifiers

FT Misc-difference 328 /note= "Wild-type Ala substituted with Trp"

XX US2003096401-A1.

XX 22-MAY-2003.

XX 28-NOV-2001; 2001US-00997209.

XX 28-NOV-2000; 2000US-0367370P.

XX (HUSE/) HUSE W D.

XX Huse WD;

XX WPI; 2003-786991/74.

XX Cell composition comprises non-yeast eukaryotic cells having diverse

XX population of variant nucleic acids or heterologous nucleic acid

XX fragments, useful for identifying polypeptide with optimized activity.

XX Example 11; Page; 0pp; English.

XX The invention relates to a cell composition comprising a population of

XX non-yeast eukaryotic cells containing diverse population of variant

XX nucleic acids, or heterologous nucleic acid fragments with distinct

XX species of nucleic acid fragments, where each of the variant nucleic

XX acids or heterologous nucleic acid fragments are expressed in different

XX cell and located within each cell at an identical site in the genome. The

XX invention is useful for identifying polypeptide with optimised activity

XX and for identifying a polypeptide receptor for a ligand. The present

XX sequence is human butyrylcholinesterase variant protein. This sequence is

XX used in the exemplification of the invention. Note: This sequence is not

XX shown in the specification but is derived from the human

XX butyrylcholinesterase wild-type protein (ABW00695) shown in figure 8 of

XX the specification

XX Sequence 574 AA;

Query Match 100.0%; Score 3110; DB 7; Length 574;

Best Local Similarity 100.0%; Pred. No. 2.2e-278; Indels 0; Gaps 0;

Matches 574; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 EDDIIATKNGKVGKNTLVFGITVTAFLGIPYAOPIGLRLEFKKQSLITKMSDIWNAIK 60

1 EDDIIATKNGKVGKNTLVFGITVTAFLGIPYAOPIGLRLEFKKQSLITKMSDIWNAIK 60

61 YANSCCONIDQSPFGHSEMMNPNTDSEDCLYLNWVTPAKPKNAATLVIYGGGQOT 120

61 YANSCCONIDQSPFGHSEMMNPNTDSEDCLYLNWVTPAKPKNAATLVIYGGGQOT 120

QY 121 GTSSLHYVDGKFLAVERIVVSNMYRVGALGFLALPGNPEAPGNMGLFDQQLALQWQK 180

DB 121 GTSSLHYVDGKFLAVERIVVSNMYRVGALGFLALPGNPEAPGNMGLFDQQLALQWQK 180

QY 181 NIAAFGPNKSVTLFGESAGAAVSGLHLSRQSHSLFTRAILIQSGSFNAFPAVTSLYEAR 240

DB 181 NIAAFGPNKSVTLFGESAGAAVSGLHLSRQSHSLFTRAILIQSGSFNAFPAVTSLYEAR 240

QY 241 NRTLNIAKLGTGSRNEMETIICLRNKDPOEILNEAFVPGTPLSYNFGPTVDGDEL 300

DB 241 NRTLNIAKLGTGSRNEMETIICLRNKDPOEILNEAFVPGTPLSYNFGPTVDGDEL 300

QY 301 DMPDILIELGQFKKQIILVGNKDEGTWFLVYGAPGFSKDNNSITTRKEFOGLKIFPPG 360

DB 301 DMPDILIELGQFKKQIILVGNKDEGTWFLVYGAPGFSKDNNSITTRKEFOGLKIFPPG 360

QY 361 VSEFGKESILFHYTWDQRPENYREALGVGYNFICPALFTFKKFSKGNNAFFY 420

DB 361 VSEFGKESILFHYTWDQRPENYREALGVGYNFICPALFTFKKFSKGNNAFFY 420

QY 421 FEHRSSKLPMPGVMGVEIEFVFGPLPERDNTYKAELISRIYKMANFAKYGNP 480

DB 421 FEHRSSKLPMPGVMGVEIEFVFGPLPERDNTYKAELISRIYKMANFAKYGNP 480

QY 481 NETONNSTMPVFKSTQRYTLTNTSTRIMTKRAQOCRFMTSPFKYLEMTGNIDEAE 540

DB 481 NETONNSTMPVFKSTQRYTLTNTSTRIMTKRAQOCRFMTSPFKYLEMTGNIDEAE 540

QY 541 WEWKAQFHRMNNYMDKNOFNDYTSKESCVGL 574

DB 541 WEWKAQFHRMNNYMDKNOFNDYTSKESCVGL 574

## RESULT 2

AA018897 standard; protein; 602 AA.

AA018897;

02-DEC-2002 (first entry)

Human butyrylcholinesterase variant #1.

Human; butyrylcholinesterase; enzyme; mutant; cocaine hydrolysis;

cocaine addition; antidiabetic; antidote.

XX Homo sapiens.

XX WO200264796-A2.

XX 22-AUG-2002.

XX 21-DEC-2001; 2001WO-US050450.

XX 26-DEC-2000; 2000US-00748739.

XX 20-DEC-2001; 2001US-00032233.

XX (MOL- ) APPLIED MOLECULAR EVOLUTION INC.

XX (UNNE-) UNIV NEBRASKA MEDICAL CENT.

XX Lockridge O, Watkins JD, Pancook JD;

XX WPI; 2002-636633/68.

XX N-PSDB; AAL49276.

XX New human butyrylcholinesterase variant polypeptides, useful for treating

XX cocaine-induced conditions.

XX Claim 1; Fig 1; 150p; English.

XX The present invention relates to mutants of human butyrylcholinesterase.

XX The enzymes have an increased cocaine hydrolysis activity and can be used

CC for treating a cocaine-induced condition. The present sequence is a  
 CC protein shown in the exemplification of the invention  
 CC  
 CC  
 CC Sequence 602 AA;

Query Match 100.0%; Score 3110; DB 5; Length 602;  
 Best Local Similarity 100.0%; Pred. No. 2,4e-278;  
 Matches 574; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDDIIATKNGKVRGMNLTVFGGTVTAFLGIPYAOPGLGRFKPKPSLTWKMSDINWATK 60  
 DB 29 EDDIIATKNGKVRGMNLTVFGGTVTAFLGIPYAOPGLGRFKPKPSLTWKMSDINWATK 88  
 QY 61 YANSCCNIDQSPFGHSGEMNPNPTDLSBDCLYLWVWIPAPKPKATVLIWYGGGFQ 120  
 DB 89 YANSCCNIDQSPFGHSGEMNPNPTDLSBDCLYLWVWIPAPKPKATVLIWYGGGFQ 146  
 QY 121 GTSSLHYDQKFLARVERVIVSMNRYVAGLGFALPGNPAQNGMLPQOQALQWVOK 180  
 DB 149 GTSSLHYDQKFLARVERVIVSMNRYVAGLGFALPGNPAQNGMLPQOQALQWVOK 208  
 QY 181 NIAAFGNPKSVTLFGESAGAASVSLHLSPGSHSLFTRAILQSGSFNAAPVATSLYEAR 240  
 DB 209 NIAAFGNPKSVTLFGESAGAASVSLHLSPGSHSLFTRAILQSGSFNAAPVATSLYEAR 268  
 QY 241 NRTLNTAKLTGCSRENETEIIKCLRNDPOEILINAEFVVPYGTPLSVNFGPTVDGDFLT 300  
 DB 269 NRTLNTAKLTGCSRENETEIIKCLRNDPOEILINAEFVVPYGTPLSVNFGPTVDGDFLT 328  
 QY 301 DMPDIIILEGQPKKTQILVGNKDEGTWFLVYGAPGSKDNNSTITRKEFOGLKIFPPG 360  
 DB 329 DMPDIIILEGQPKKTQILVGNKDEGTWFLVYGAPGSKDNNSTITRKEFOGLKIFPPG 388  
 QY 361 VSEFGKESILFHTDWDQDQRPENYRALGDVVDYVFCIPALEFTKFKFSWGNNAFFY 420  
 DB 389 VSEFGKESILFHTDWDQDQRPENYRALGDVVDYVFCIPALEFTKFKFSWGNNAFFY 448  
 QY 421 FEHRSSKLPWPEWNGVWGHYEIEFVFGPLERDNTYKAEIISRSIVKMANPAKXGNP 480  
 DB 449 FEHRSSKLPWPEWNGVWGHYEIEFVFGPLERDNTYKAEIISRSIVKMANPAKXGNP 508  
 QY 481 NETONNSTWPFVKSTQKTLTNTBSTRTIMTKLRAOQCRFWTSFPKVLGMTGNIDEAE 540  
 DB 509 NETONNSTWPFVKSTQKTLTNTBSTRTIMTKLRAOQCRFWTSFPKVLGMTGNIDEAE 568  
 QY 541 WEWKAGFHRNNNYMMDKNQFNDYTSKESCVGL 574  
 DB 569 WEWKAGFHRNNNYMMDKNQFNDYTSKESCVGL 602

## RESULT 3

ID ADR01039 standard; protein; 574 AA.

AC ADR01039;

DT 23-SEP-2004 (first entry)

DE Human butyrylcholinesterase A328W/V331L variant.

XX butyrylcholinesterase; cocaine-induced condition;  
 KM cocaine-based butyrylcholinesterase substrate; cocaine-overdose;  
 KW cocaine addiction; human; butyrylcholinesterase variant.

OS Homo sapiens.

OS Synthetic.

PN US2004121970-A1.

PD 24-JUN-2004.

PF 20-DEC-2002; 2002US-00324466.

PR 20-DEC-2002; 2002US-00324466.

XX (WATK/) WATKINS J D.  
 PA (PANCO/) PANCOCK J D.

XX WATKINS JD, PancoCK JD;

XX WPI; 2004-468195/44.  
 DR N-PSDB; ADR01039.

PT New butyrylcholinesterase variant polypeptide, useful in treating cocaine  
 PT -induced condition, i.e. cocaine-overdose or cocaine addiction.

XX Claim 1; SEQ ID NO 6; 131pp; English.

XX The invention describes a butyrylcholinesterase variant polypeptide (I)  
 CC comprising any of the 21 sequences of 57 amino acids each (EVEN SEQ ID  
 CC NOS: 2-42) or their functional fragments. Also described are: a nucleic  
 CC acid encoding (I) comprising any of the 21 nucleic acid sequences of 2416  
 CC bp each (ODD SEQ ID NOS: 1-41) or their fragments; a method of treating a  
 CC cocaine-induced condition; and a method of hydrolyzing a cocaine-based  
 CC butyrylcholinesterase substrate. (I) is butyrylcholinesterase variant  
 CC polypeptide comprising any of the 21 sequences of 57 amino acids each  
 CC (EVEN SEQ ID NOS: 2-42), encoded by a nucleic acid comprising any of the  
 CC 21 nucleic acid sequences of 2416 bp each (ODD SEQ ID NOS: 1-41). The  
 CC butyrylcholinesterase variant polypeptides and nucleic acids and methods  
 CC are useful in treating cocaine-induced condition i.e. cocaine-overdose or  
 CC cocaine addiction. This is the amino acid sequence of a human  
 CC butyrylcholinesterase variant.

XX Sequence 574 AA;

Query Match 99.9%; Score 3107; DB 8; Length 574;  
 Best Local Similarity 99.8%; Pred. No. 4,2e-278;  
 Matches 573; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDDIIATKNGKVRGMNLTVFGGTVTAFLGIPYAOPGLGRFKPKPSLTWKMSDINWATK 60  
 DB 1 EDDIIATKNGKVRGMNLTVFGGTVTAFLGIPYAOPGLGRFKPKPSLTWKMSDINWATK 60  
 QY 61 YANSCCNIDQSPFGHSGEMNPNPTDLSBDCLYLWVWIPAPKPKATVLIWYGGGFQ 120  
 DB 61 YANSCCNIDQSPFGHSGEMNPNPTDLSBDCLYLWVWIPAPKPKATVLIWYGGGFQ 120  
 QY 121 GTSSLHYDQKFLARVERVIVSMNRYVAGLGFALPGNPAQNGMLPQOQALQWVOK 180  
 DB 121 GTSSLHYDQKFLARVERVIVSMNRYVAGLGFALPGNPAQNGMLPQOQALQWVOK 180  
 QY 181 NIAAFGNPKSVTLFGESAGAASVSLHLSPGSHSLFTRAILQSGSFNAAPVATSLYEAR 240  
 DB 181 NIAAFGNPKSVTLFGESAGAASVSLHLSPGSHSLFTRAILQSGSFNAAPVATSLYEAR 240  
 QY 241 NRTLNTAKLTGCSRENETEIIKCLRNDPOEILINAEFVVPYGTPLSVNFGPTVDGDFLT 300  
 DB 241 NRTLNTAKLTGCSRENETEIIKCLRNDPOEILINAEFVVPYGTPLSVNFGPTVDGDFLT 300  
 QY 301 DMPDIIILEGQPKKTQILVGNKDEGTWFLVYGAPGSKDNNSTITRKEFOGLKIFPPG 360  
 DB 301 DMPDIIILEGQPKKTQILVGNKDEGTWFLVYGAPGSKDNNSTITRKEFOGLKIFPPG 360  
 QY 361 VSEFGKESILFHTDWDQDQRPENYRALGDVVDYVFCIPALEFTKFKFSWGNNAFFY 420  
 DB 361 VSEFGKESILFHTDWDQDQRPENYRALGDVVDYVFCIPALEFTKFKFSWGNNAFFY 420  
 QY 421 FEHRSSKLPWPEWNGVWGHYEIEFVFGPLERDNTYKAEIISRSIVKMANPAKXGNP 480  
 DB 421 FEHRSSKLPWPEWNGVWGHYEIEFVFGPLERDNTYKAEIISRSIVKMANPAKXGNP 480  
 QY 481 NETONNSTWPFVKSTQKTLTNTBSTRTIMTKLRAOQCRFWTSFPKVLGMTGNIDEAE 540  
 DB 481 NETONNSTWPFVKSTQKTLTNTBSTRTIMTKLRAOQCRFWTSFPKVLGMTGNIDEAE 540  
 QY 541 WEWKAGFHRNNNYMMDKNQFNDYTSKESCVGL 574

DB 541 WEKAGFHRMNNYMDWKQFNDYTSKESCVGL 574

RESULT 4  
ADRO1047  
ID ADRO1047 standard; protein; 574 AA.  
AC ADRO1047;  
XX 23-SEP-2004 (first entry)  
DE Human butyrylcholinesterase A328W/S287G/A199S variant.  
XX butyrylcholinesterase; cocaine-induced condition;  
KM cocaine-based butyrylcholinesterase substrate; cocaine-overdose;  
XX cocaine addiction; human; butyrylcholinesterase variant.  
OS Homo sapiens.  
OS Synthetic.  
XX US2004121970-A1.  
XX 24-JUN-2004.  
XX 20-DEC-2002; 2002US-00324466.  
XX 20-DEC-2002; 2002US-00324466.  
XX (WATK/) WATKINS J D.  
XX (PANC/) PANCOCK J D.  
XX WATKINS JD, Pancook JD;  
XX WPI; 2004-468195/44.  
XX N-PSDB; ADRO1046.  
XX New butyrylcholinesterase variant polypeptide, useful in treating cocaine  
PT -induced condition, i.e. cocaine-overdose or cocaine addiction.  
XX Claim 1; SEQ ID NO 14; 131pp; English.  
XX The invention describes a butyrylcholinesterase variant polypeptide (I)  
XX comprising any of the 21 sequences of 57 amino acids each (EVEN SEQ ID  
XX NOS: 2-42) or their functional fragments. Also described are: a nucleic  
XX acid encoding (I) comprising any of the 21 nucleic acid sequences of 2416  
XX bp each (ODD SEQ ID NOS: 1-41) or their fragments; a method of treating a  
XX cocaine-induced condition; and a method of hydrolysing a cocaine-based  
XX butyrylcholinesterase substrate. (I) is butyrylcholinesterase variant  
XX polypeptide comprising any of the 21 sequences of 57 amino acids each  
XX (EVEN SEQ ID NOS: 2-42), encoded by a nucleic acid comprising any of the  
XX 21 nucleic acid sequences of 2416 bp each (ODD SEQ ID NOS: 1-41). The  
XX butyrylcholinesterase variant polypeptides and nucleic acids and methods  
XX are useful in treating cocaine-induced condition i.e. cocaine-overdose or  
XX cocaine addiction. This is the amino acid sequence of a human  
XX butyrylcholinesterase variant.  
XX Sequence 574 AA;  
SQ

Query Match 99.8%; Score 3103; DB 8; Length 574;  
Best Local Similarity 99.7%; Pred. No. 9.9e-278;  
Matches 572; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDDIIITATKNGKVMNLTIVGGYTAFLGIPYQPPGRIRFKKPSQSLTWSQIWNATK 60  
DB 1 EDDIIITATKNGKVMNLTIVGGYTAFLGIPYQPPGRIRFKKPSQSLTWSQIWNATK 60  
QY 61 YANSCCQINDSPFGFSGEMNPNVTDISEDCVYNWVIRPKPKNATVLTIWGGGQOT 120  
DB 61 YANSCCQINDSPFGFSGEMNPNVTDISEDCVYNWVIRPKPKNATVLTIWGGGQOT 120  
QY 121 GTSSLIHVDDGKFLARVERIVVSMNRYGALGFLALPGNPEAPGNMGLFDQOLALQWYOK 180  
DB 121 GTSSLIHVDDGKFLARVERIVVSMNRYGALGFLALPGNPEAPGNMGLFDQOLALQWYOK 180

DB 121 GTSSLIHVDDGKFLARVERIVVSMNRYGALGFLALPGNPEAPGNMGLFDQOLALQWYOK 180  
QY 181 NTAAREGNPKSVTLTGESAGASVSLHLSPGSHSLFTFALIIQSGSPNAPMAVTSLEYAR 240  
DB 181 NTAAREGNPKSVTLTGESAGASVSLHLSPGSHSLFTFALIIQSGSPNAPMAVTSLEYAR 240  
QY 241 NRTLANLAKLTGCSRENETEIIKCLRNKDPQELLNEAFVVPYGTPLSVNFGPTVDGFLT 300  
DB 241 NRTLANLAKLTGCSRENETEIIKCLRNKDPQELLNEAFVVPYGTPLSVNFGPTVDGFLT 300  
QY 301 DMPDILLEIGQFKQTQIIVGVNKDEGTWFLVYGAPGFSKDNNSIITRKEFOGLKIFPG 360  
DB 301 DMPDILLEIGQFKQTQIIVGVNKDEGTWFLVYGAPGFSKDNNSIITRKEFOGLKIFPG 360  
QY 361 VSEFGKESILFHYTVDVDPORPENYREALGDVVDNFCPLAEFTKFSSEGNNAFFYX 420  
DB 361 VSEFGKESILFHYTVDVDPORPENYREALGDVVDNFCPLAEFTKFSSEGNNAFFYX 420  
QY 421 FEHRSSKLPMPPEWGMVGHYEIEFVFGPLPERRDNTYKAELLRSIVKRMANFATYGNP 480  
DB 421 FEHRSSKLPMPPEWGMVGHYEIEFVFGPLPERRDNTYKAELLRSIVKRMANFATYGNP 480  
QY 481 NETONNSTSWPVFKSTEQKYLTLNTRSTRIMTKLRACQCRFMTSPFPKYLEMTGNIDAE 540  
DB 481 NETONNSTSWPVFKSTEQKYLTLNTRSTRIMTKLRACQCRFMTSPFPKYLEMTGNIDAE 540  
QY 541 WEKAGFHRMNNYMDWKQFNDYTSKESCVGL 574  
DB 541 WEKAGFHRMNNYMDWKQFNDYTSKESCVGL 574

RESULT 5  
ADRO1051  
ID ADRO1051 standard; protein; 574 AA.  
XX ADRO1051;  
XX 23-SEP-2004 (first entry)  
DE Human butyrylcholinesterase A328W/F227A variant.  
XX butyrylcholinesterase; cocaine-induced condition;  
KM cocaine-based butyrylcholinesterase substrate; cocaine-overdose;  
XX cocaine addiction; human; butyrylcholinesterase variant.  
OS Homo sapiens.  
OS Synthetic.  
XX US2004121970-A1.  
XX 24-JUN-2004.  
XX 20-DEC-2002; 2002US-00324466.  
XX 20-DEC-2002; 2002US-00324466.  
XX (WATK/) WATKINS J D.  
XX (PANC/) PANCOCK J D.  
XX WATKINS JD, Pancook JD;  
XX WPI; 2004-468195/44.  
XX N-PSDB; ADRO1050.  
XX New butyrylcholinesterase variant polypeptide, useful in treating cocaine  
PT -induced condition, i.e. cocaine-overdose or cocaine addiction.  
XX Claim 1; SEQ ID NO 18; 131pp; English.  
XX The invention describes a butyrylcholinesterase variant polypeptide (I)  
XX comprising any of the 21 sequences of 57 amino acids each (EVEN SEQ ID  
XX NOS: 2-42) or their functional fragments. Also described are: a nucleic  
XX acid encoding (I) comprising any of the 21 nucleic acid sequences of 2416



CC bp each (ODD SEQ ID NOS: 1-41) or their fragments; a method of treating a  
CC cocaine-induced condition; and a method of hydrolysing a cocaine-based  
CC butyrylcholinesterase substrate. (1) is butyrylcholinesterase variant  
CC polypeptide comprising any of the 21 sequences of 57 amino acids each  
CC (EVEN SEQ ID NOS: 2-42), encoded by a nucleic acid comprising any of the  
CC 21 nucleic acid sequences of 2416 bp each (ODD SEQ ID NOS: 1-41). The  
CC butyrylcholinesterase variant polypeptides and nucleic acids and methods  
CC are useful in treating cocaine-induced condition i.e. cocaine-overdose or  
CC cocaine addiction. This is the amino acid sequence of a human  
CC butyrylcholinesterase variant.

XX Sequence 574 AA;

Query Match 99.7%; Score 3102; DB 8; Length 574;  
Best Local Similarity 99.8%; Pred. No. 1.2e-277;  
Matches 573; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDDIIATKNGKRGKGNLTVFGGTVAFLGIPYAPPLGLRFPKPSQSLTKMSDINWATK 60  
DB 1 EDDIIATKNGKRGKGNLTVFGGTVAFLGIPYAPPLGLRFPKPSQSLTKMSDINWATK 60  
QY 61 YANSCCONIDQSPFGHSEMMNPNTDLSBDCLYLAWMIPAPKRNATVLIWYGGGFQT 120  
DB 61 YANSCCONIDQSPFGHSEMMNPNTDLSBDCLYLAWMIPAPKRNATVLIWYGGGFQT 120  
QY 121 GTSSLAHYDQKFLARVERVIVSMNYRVGALGFLALPGNEAPGNMGLFPQOLALQWVOK 180  
DB 121 GTSSLAHYDQKFLARVERVIVSMNYRVGALGFLALPGNEAPGNMGLFPQOLALQWVOK 180  
QY 181 NIAAFGNPKSVTLFGESAGAAVSJLHLSPGSHSLFTRAILQSGSFNAWAATVSYEAR 240  
DB 181 NIAAFGNPKSVTLFGESAGAAVSJLHLSPGSHSLFTRAILQSGSFNAWAATVSYEAR 240  
QY 241 NRTLNIAKLTCGSENETEIIKCLRNDPOEILINAEFVVPYGPPLSVNGPTDGPFLT 300  
DB 241 NRTLNIAKLTCGSENETEIIKCLRNDPOEILINAEFVVPYGPPLSVNGPTDGPFLT 300  
QY 301 DMPDILILEQFKKTOILVGNKDEGTWFLVYGAPGSKDNNSIITRKEFOEGLKIFPPG 360  
DB 301 DMPDILILEQFKKTOILVGNKDEGTWFLVYGAPGSKDNNSIITRKEFOEGLKIFPPG 360  
QY 361 VSEFGKESILFHYTDWDDORPENYREALGDVVDYVNICPALEFTYKKSSEMGNAFFY 420  
DB 361 VSEFGKESILFHYTDWDDORPENYREALGDVVDYVNICPALEFTYKKSSEMGNAFFY 420  
QY 421 FEHRSSKLPWPEWGVHGYEIEFVGLPLERRDNYTKAEIISRSIVKMANPAKYGNP 480  
DB 421 FEHRSSKLPWPEWGVHGYEIEFVGLPLERRDNYTKAEIISRSIVKMANPAKYGNP 480  
QY 481 NETQNNSTWVPFSTROKYLTLNTESTRIIMTKLRAOQCRFWTSFPFKVLMTGNDIEAE 540  
DB 481 NETQNNSTWVPFSTROKYLTLNTESTRIIMTKLRAOQCRFWTSFPFKVLMTGNDIEAE 540  
QY 541 MEMKAGFHRMNNYMMDKNQFNQDYSKESCVGL 574  
DB 541 MEMKAGFHRMNNYMMDKNQFNQDYSKESCVGL 574

RESULT 6  
ADRO1035 ID ADRO1035 standard; protein; 574 AA.

XX AC ADRO1035;

XX DT 23-SEP-2004 (first entry)

XX DE Human butyrylcholinesterase A328W/Y332M variant.

XX KM butyrylcholinesterase; cocaine-induced condition;  
KM cocaine-based butyrylcholinesterase substrate; cocaine-overdose;  
KW cocaine addiction; human; butyrylcholinesterase variant.

XX OS Homo sapiens.

OS Synthetic.

XX US2004121970-A1.

XX 24-JUN-2004.

XX 20-DEC-2002; 2002US-00324466.

XX 20-DEC-2002; 2002US-00324466.

XX (WATK/) WATKINS J D.

XX (PANC/) PANCOCK J D.

XX WPI: 2004-468195/44.

XX N-PSDB; ADRO1034.

XX New butyrylcholinesterase variant polypeptide, useful in treating cocaine  
XX -induced condition, i.e. cocaine-overdose or cocaine addiction.

XX Claim 1; SEQ ID NO 2; 133bp; English.

XX The invention describes a butyrylcholinesterase variant polypeptide (1)  
XX comprising any of the 21 sequences of 57 amino acids each (EVEN SEQ ID  
XX NOS: 2-42) or their functional fragments. Also described are: a nucleic  
XX acid encoding (1) comprising any of the 21 nucleic acid sequences of 2416  
XX bp each (ODD SEQ ID NOS: 1-41) or their fragments; a method of treating a  
XX cocaine-induced condition; and a method of hydrolysing a cocaine-based  
XX butyrylcholinesterase substrate. (1) is butyrylcholinesterase variant  
XX polypeptide comprising any of the 21 sequences of 57 amino acids each  
XX (EVEN SEQ ID NOS: 2-42), encoded by a nucleic acid comprising any of the  
XX 21 nucleic acid sequences of 2416 bp each (ODD SEQ ID NOS: 1-41). The  
XX butyrylcholinesterase variant polypeptides and nucleic acids and methods  
XX are useful in treating cocaine-induced condition i.e. cocaine-overdose or  
XX cocaine addiction. This is the amino acid sequence of a human  
XX butyrylcholinesterase variant.

XX Sequence 574 AA;

Query Match 99.7%; Score 3102; DB 8; Length 574;  
Best Local Similarity 99.8%; Pred. No. 1.2e-277;  
Matches 573; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDDIIATKNGKRGKGNLTVFGGTVAFLGIPYAPPLGLRFPKPSQSLTKMSDINWATK 60  
DB 1 EDDIIATKNGKRGKGNLTVFGGTVAFLGIPYAPPLGLRFPKPSQSLTKMSDINWATK 60  
QY 61 YANSCCONIDQSPFGHSEMMNPNTDLSBDCLYLAWMIPAPKRNATVLIWYGGGFQT 120  
DB 61 YANSCCONIDQSPFGHSEMMNPNTDLSBDCLYLAWMIPAPKRNATVLIWYGGGFQT 120  
QY 121 GTSSLAHYDQKFLARVERVIVSMNYRVGALGFLALPGNEAPGNMGLFPQOLALQWVOK 180  
DB 121 GTSSLAHYDQKFLARVERVIVSMNYRVGALGFLALPGNEAPGNMGLFPQOLALQWVOK 180  
QY 181 NIAAFGNPKSVTLFGESAGAAVSJLHLSPGSHSLFTRAILQSGSFNAWAATVSYEAR 240  
DB 181 NIAAFGNPKSVTLFGESAGAAVSJLHLSPGSHSLFTRAILQSGSFNAWAATVSYEAR 240  
QY 241 NRTLNIAKLTCGSENETEIIKCLRNDPOEILINAEFVVPYGPPLSVNGPTDGPFLT 300  
DB 241 NRTLNIAKLTCGSENETEIIKCLRNDPOEILINAEFVVPYGPPLSVNGPTDGPFLT 300  
QY 301 DMPDILILEQFKKTOILVGNKDEGTWFLVYGAPGSKDNNSIITRKEFOEGLKIFPPG 360  
DB 301 DMPDILILEQFKKTOILVGNKDEGTWFLVYGAPGSKDNNSIITRKEFOEGLKIFPPG 360  
QY 361 VSEFGKESILFHYTDWDDORPENYREALGDVVDYVNICPALEFTYKKSSEMGNAFFY 420  
DB 361 VSEFGKESILFHYTDWDDORPENYREALGDVVDYVNICPALEFTYKKSSEMGNAFFY 420  
QY 421 FEHRSSKLPWPEWGVHGYEIEFVGLPLERRDNYTKAEIISRSIVKMANPAKYGNP 480

```
DB 421 FEHRSSTLPWPEMGMVHGEIEFVGLERDRNTYKAEILSRIVKMANPAKYGNP 480
QY 481 NETONNSTSWPVFKSTEQKYLTLNTESTRIMTKLRADQOCRFMTSPFKYLEMTGNIDEAE 540
DB 481 NETONNSTSWPVFKSTEQKYLTLNTESTRIMTKLRADQOCRFMTSPFKYLEMTGNIDEAE 540
QY 541 MEMKAGFHRNNYMMDMKNOFNDYTSKESCVGL 574
DB 541 MEMKAGFHRNNYMMDMKNOFNDYTSKESCVGL 574

RESULT 7
ADRO1041
ID ADRO1041 standard; protein; 574 AA.
XX
AC ADRO1041;
XX
DT 23-SEP-2004 (first entry)
XX
DE Human butyrylcholinesterase A328W/Y332S variant.
XX
DE butyrylcholinesterase; cocaine-induced condition;
XX
KW cocaine-based butyrylcholinesterase substrate; cocaine-overdose;
XX
KW cocaine addiction; human; butyrylcholinesterase variant.
XX
OS Homo sapiens.
XX
OS Synthetic.
XX
PN US2004121970-A1.
XX
PD 24-JUN-2004.
XX
PF 20-DEC-2002; 2002US-00324466.
XX
PR 20-DEC-2002; 2002US-00324466.
XX
PA (WATK/) WATKINS J D.
XX
PA (PANC/) PANCOCK J D.
XX
PI Watkins JD, Pancook JD;
XX
DR WPI, 2004-468195/44.
XX
DR N-PSDB; ADRO1040.
XX
PT New butyrylcholinesterase variant polypeptide, useful in treating cocaine
PT -induced condition, i.e. cocaine-overdose or cocaine addiction.
XX
PS Claim 1; SEQ ID NO 8; 131bp; English.
XX
XX The invention describes a butyrylcholinesterase variant polypeptide (1)
XX comprising any of the 21 sequences of 57 amino acids each (EVEN SEQ ID
XX NOS: 2-42) or their functional fragments. Also described are: a nucleic
XX acid encoding (1) comprising any of the 21 nucleic acid sequences of 2416
XX bp each (ODD SEQ ID NOS: 1-41) or their fragments; a method of treating a
XX cocaine-induced condition; and a method of hydrolysing a cocaine-based
XX butyrylcholinesterase substrate. (1) is butyrylcholinesterase variant
XX butyrylcholinesterase comprising any of the 21 sequences of 57 amino acids each
XX (EVEN SEQ ID NOS: 2-42), encoded by a nucleic acid comprising any of the
XX 21 nucleic acid sequences of 2416 bp each (ODD SEQ ID NOS: 1-41). The
XX butyrylcholinesterase variant polypeptides and nucleic acids and methods
XX are useful in treating cocaine-induced condition i.e. cocaine-overdose or
XX cocaine addiction. This is the amino acid sequence of a human
XX butyrylcholinesterase variant.
XX
SQ Sequence 574 AA;
XX
Query Match 99.7%; Score 3101; DB 8; Length 574;
Best Local Similarity 99.8%; Pred. No. 1.5e-277;
Matches 573; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 EDDIIATKNGKVRGNMLTFGGTVTAFLGIPVAGPPLGRLEFKKRPQSLTKMSDIMNATK 60
|||||
```

```
DB 1 EDDIIATKNGKVRGNMLTFGGTVTAFLGIPVAGPPLGRLEFKKRPQSLTKMSDIMNATK 60
QY 61 YANSCCNIDQSPFGTHGSEMMNPNTDLSDDCLYLNWVI PAKPKNATYLIWYGGGFGOT 120
DB 61 YANSCCNIDQSPFGTHGSEMMNPNTDLSDDCLYLNWVI PAKPKNATYLIWYGGGFGOT 120
QY 121 GTSLSIHYDDKFLARVERVIVVSMNRYVGLGFLALPGNPEAPGNKGLFDQOLALQWVK 180
DB 121 GTSLSIHYDDKFLARVERVIVVSMNRYVGLGFLALPGNPEAPGNKGLFDQOLALQWVK 180
QY 181 NIAAFGNPKSVTLFGESAGAAVSLSLSPGSHSLFTRAILLOSGFNAPMAYTSIYEAR 240
DB 181 NIAAFGNPKSVTLFGESAGAAVSLSLSPGSHSLFTRAILLOSGFNAPMAYTSIYEAR 240
QY 241 NRTNLIAKLTGCSRENETEIIKCLRNDPOEILINBAFVVPYGTPLSVNFGPTVDDPFLT 300
DB 241 NRTNLIAKLTGCSRENETEIIKCLRNDPOEILINBAFVVPYGTPLSVNFGPTVDDPFLT 300
QY 301 DMPDILLELGQFKKTOILVGNKDEGTWFLVYGAPGSKUNNSITTRKEFOEGLKIFEPG 360
DB 301 DMPDILLELGQFKKTOILVGNKDEGTWFLVYGAPGSKUNNSITTRKEFOEGLKIFEPG 360
QY 361 VSEFGKESILFHYTDWDDQRPENYREALGDVGDYNICPALFTKKEFSEMGNNAFYY 420
DB 361 VSEFGKESILFHYTDWDDQRPENYREALGDVGDYNICPALFTKKEFSEMGNNAFYY 420
QY 421 FEHRSSTLPWPEMGMVHGEIEFVGLERDRNTYKAEILSRIVKMANPAKYGNP 480
DB 421 FEHRSSTLPWPEMGMVHGEIEFVGLERDRNTYKAEILSRIVKMANPAKYGNP 480
QY 481 NETONNSTSWPVFKSTEQKYLTLNTESTRIMTKLRADQOCRFMTSPFKYLEMTGNIDEAE 540
DB 481 NETONNSTSWPVFKSTEQKYLTLNTESTRIMTKLRADQOCRFMTSPFKYLEMTGNIDEAE 540
QY 541 MEMKAGFHRNNYMMDMKNOFNDYTSKESCVGL 574
DB 541 MEMKAGFHRNNYMMDMKNOFNDYTSKESCVGL 574

RESULT 8
ADRO1037
ID ADRO1037 standard; protein; 574 AA.
XX
AC ADRO1037;
XX
DT 23-SEP-2004 (first entry)
XX
DE Human butyrylcholinesterase A328W/Y332P variant.
XX
DE butyrylcholinesterase; cocaine-induced condition;
XX
KW cocaine-based butyrylcholinesterase substrate; cocaine-overdose;
XX
KW cocaine addiction; human; butyrylcholinesterase variant.
XX
OS Homo sapiens.
XX
OS Synthetic.
XX
PN US2004121970-A1.
XX
PD 24-JUN-2004.
XX
PF 20-DEC-2002; 2002US-00324466.
XX
PR 20-DEC-2002; 2002US-00324466.
XX
PA (WATK/) WATKINS J D.
XX
PA (PANC/) PANCOCK J D.
XX
PI Watkins JD, Pancook JD;
XX
DR WPI, 2004-468195/44.
XX
DR N-PSDB; ADRO1036.
XX
PT New butyrylcholinesterase variant polypeptide, useful in treating cocaine
```





FT Region 277..289  
 FT /note= "Region used to generate focussed libraries"  
 FT Region 327..332  
 FT /note= "Region used to generate focussed libraries"  
 FT Active-site 329  
 FT /note= "Aromatic active site gorge residue"  
 FT Active-site 332  
 FT /note= "Aromatic active site gorge residue"  
 FT Disulfide-bond 400..519  
 FT Region 429..442  
 FT /note= "Region used to generate focussed libraries"  
 FT Active-site 430  
 FT /note= "Aromatic active site gorge residue"  
 FT Active-site 440  
 FT /note= "Aromatic active site gorge residue"  
 FT MO200244361-A2.  
 PD 06-JUN-2002.  
 XX 28-NOV-2001; 2001WO-US044600.  
 PF 28-NOV-2000; 2000US-00724762.  
 XX  
 PR (MOLE-) APPLIED MOLECULAR EVOLUTION INC.  
 PA Huse WD;  
 PI WPI; 2002-519586/55.  
 XX  
 DR New cell composition having population of non-yeast eukaryotic cells  
 XX containing diverse population of variant nucleic acids that are expressed  
 PT in different cell and located within each cell at identical site in  
 PT genome.  
 XX  
 XX Example 11; Page 155-156; 157pp; English.  
 PS  
 XX The present invention relates to a cell composition having population of  
 CC non-yeast eukaryotic cells containing a diverse population of ten or more  
 CC variant nucleic acids or heterologous nucleic acid fragments comprising  
 CC distinct species of nucleic acid fragments, each of the variant nucleic  
 CC acids or heterologous nucleic acid fragments being expressed in different  
 CC cells and located within each cell at an identical site in the genome.  
 CC The composition is useful to identify polypeptides exhibiting optimised  
 CC activity. It is also useful for identifying a binding ligand. It is also  
 CC useful for identifying specific ligands to desired target molecules. Such  
 CC ligands can be developed as potential drug candidates or alternatively  
 CC used as lead compounds for the generation and identification of ligand  
 CC variants which exhibit enhanced activity of the desired binding property.  
 CC The methods can similarly be applied to identify a nucleic acid having an  
 CC optimised activity by screening for an activity associated with a parent  
 CC nucleic acid. The present sequence is human butyrylcholinesterase  
 CC protein. This sequence is used in the exemplification of the invention  
 CC  
 CC  
 CC Sequence 574 AA;  
 SQ  
 Query Match 99.5%; Score 3096; DB 5; Length 574;  
 Best Local Similarity 99.8%; Pred. No. 4.4e-277;  
 Matches 573; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 181 NIAAFGNPKSVTLFGESAGAASVSLHLSPGSHSLFTRAILQSGSFNAFWATSLYEAR 240  
 Qy 241 NRTNLAKLTGCGSENETETIKLRNDPOEILLNEAFVYPGTPLSVNPFTVDGDFLT 300  
 Db 241 NRTNLAKLTGCGSENETETIKLRNDPOEILLNEAFVYPGTPLSVNPFTVDGDFLT 300  
 Qy 301 DMPDILLELQGFKKYQLLVGNKDEGTPLVYGA PGFSKDNNSITRKEROGLKIFPPG 360  
 Db 301 DMPDILLELQGFKKYQLLVGNKDEGTPLVYGA PGFSKDNNSITRKEROGLKIFPPG 360  
 Qy 361 VSEFGKESILPHYTDWDDORPENYREALGDVYGVDFYICPALFTTKSEKGNNAFFY 420  
 Db 361 VSEFGKESILPHYTDWDDORPENYREALGDVYGVDFYICPALFTTKSEKGNNAFFY 420  
 Qy 421 FEHRSSKLPMWBMWGVHGEIEFVGLPLERRDNYKABEILSRSLVKRMANPAKYGNP 480  
 Db 421 FEHRSSKLPMWBMWGVHGEIEFVGLPLERRDNYKABEILSRSLVKRMANPAKYGNP 480  
 Qy 481 NETONNSTSWPVFKSTEOKYTLTNTBSTRIMTKLRAOQCFWTSFPFKVLEMTGNIDAE 540  
 Db 481 NETONNSTSWPVFKSTEOKYTLTNTBSTRIMTKLRAOQCFWTSFPFKVLEMTGNIDAE 540  
 Qy 541 WEMKAGFHRNNNTYMDKNOFNDYTSKESCVGL 574  
 Db 541 WEMKAGFHRNNNTYMDKNOFNDYTSKESCVGL 574  
 RESULT 12  
 AA018982  
 ID AA018982 standard; protein; 574 AA.  
 XX  
 AC AA018982;  
 XX  
 DT 02-DEC-2002 (first entry)  
 XX  
 DE Human butyrylcholinesterase mutant A328/V331L.  
 XX  
 KW Human; butyrylcholinesterase; enzyme; mutant; cocaine hydrolysis;  
 KW cocaine addiction; antiaddictive; antidote; mutain.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 FH Key Location/Qualifiers  
 FT Misc-difference 328 /note= "wild-type Ala substituted by Trp"  
 FT Misc-difference 331 /note= "wild-type Val substituted by Leu"  
 PN MO200264796-A2.  
 XX  
 XX 22-AUG-2002.  
 PD  
 PF 21-DEC-2001; 2001WO-US050450.  
 XX  
 PF 26-DEC-2000; 2000US-00748739.  
 PR 20-DEC-2001; 2001US-00032233.  
 XX  
 PA (MOLE-) APPLIED MOLECULAR EVOLUTION INC.  
 PA (UYNE-) UNIV NEBRASKA MEDICAL CENT.  
 PI Lockridge O, Watkins JD, Hancock JD;  
 XX WPI; 2002-636633/68.  
 DR  
 XX New human butyrylcholinesterase variant polypeptides, useful for treating  
 PT cocaine-induced conditions.  
 PT  
 XX Claim 1; Page; 150pp; English.  
 XX  
 CC The present invention relates to mutants of human butyrylcholinesterase.  
 CC The enzymes have an increased cocaine hydrolysis activity and can be used

CC for treating a cocaine-induced condition. The present sequence is a  
CC mutant protein shown in the exemplification of the invention

XX Sequence 574 AA;

Query Match 99.5%; Score 3096; DB 5; Length 574;  
Best Local Similarity 99.7%; Pred. No. 4.4e-277;  
Matches 572; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 EDDIIITKNGKVRGMNLTVEGGVTAFGLGIPYAPPLGRLFRKKPQSLTKMSDINMNTK 60
   |||||
DB 1 EDDIIITKNGKVRGMNLTVEGGVTAFGLGIPYAPPLGRLFRKKPQSLTKMSDINMNTK 60
QY 61 YANSCCNIDQSPFPFGHSEMMNPTDLSBDCLYANWIPAPKPNATVLIWYGGGFOT 120
   |||||
DB 61 YANSCCNIDQSPFPFGHSEMMNPTDLSBDCLYANWIPAPKPNATVLIWYGGGFOT 120
QY 121 GTSSLHYVDGKFLARVERIVVSMNYRVGALGFALPBNPAGNMGFLPDQQLALQWVOK 180
   |||||
DB 121 GTSSLHYVDGKFLARVERIVVSMNYRVGALGFALPBNPAGNMGFLPDQQLALQWVOK 180
QY 181 NIAAFGKPKSVTLFGESAGASVSLHLSFGSHSLFTRAILQSGSFNAPAVTSLYEAR 240
   |||||
DB 181 NIAAFGKPKSVTLFGESAGASVSLHLSFGSHSLFTRAILQSGSFNAPAVTSLYEAR 240
QY 241 NRTLNLAQLTGCSRENETEIIKCLRNKDPQELILNEAFVVPYGTPLSVNFGPTVDGFLT 300
   |||||
DB 241 NRTLNLAQLTGCSRENETEIIKCLRNKDPQELILNEAFVVPYGTPLSVNFGPTVDGFLT 300
QY 301 DMPDILLELGOQFKTQILVGNKDEGTWFLVYGAPGFSKDNNSIITRKEFOEGKIFPPG 360
   |||||
DB 301 DMPDILLELGOQFKTQILVGNKDEGTWFLVYGAPGFSKDNNSIITRKEFOEGKIFPPG 360
QY 361 VSEFGKESILFHYTDWVDORPENYREALGDVVDYNFICPALFTKFSWGNNAFFYY 420
   |||||
DB 361 VSEFGKESILFHYTDWVDORPENYREALGDVVDYNFICPALFTKFSWGNNAFFYY 420
QY 421 FEHRSSKLPWPBMWGVHGYEIEFVFGPLERRDNTYKAEELISRSIVKRWANFAKYNP 480
   |||||
DB 421 FEHRSSKLPWPBMWGVHGYEIEFVFGPLERRDNTYKAEELISRSIVKRWANFAKYNP 480
QY 481 NETONNSTSWPVFKSTEQKYLTLNTESTRIMTKLRAOCCRFWTSFPKYLEMTGNIDEAE 540
   |||||
DB 481 NETONNSTSWPVFKSTEQKYLTLNTESTRIMTKLRAOCCRFWTSFPKYLEMTGNIDEAE 540
QY 541 MEMKAGFHRNNNYMDMKQFNDYTSKESCVGL 574
   |||||
DB 541 MEMKAGFHRNNNYMDMKQFNDYTSKESCVGL 574

```

# RESULT 13

AAO18898 standard; protein; 574 AA.

```

XX AAO18898
XX ID AAO18898
XX AC AAO18898;
XX DT 02-DEC-2002 (first entry)
XX DE Human butyrylcholinesterase.
XX KM Human; butyrylcholinesterase; enzyme; mutant; cocaine hydrolysis;
XX KW cocaine addiction; antiaddictive; antidote.
XX OS Homo sapiens.
XX PN WO200264796-A2.
XX PD 22-AUG-2002.
XX PF 21-DEC-2001; 2001MO-US050450.
XX PR 26-DEC-2000; 2000US-00748739.
XX PR 20-DEC-2001; 2001US-00032233.

```

XX (MOLE-) APPLIED MOLECULAR EVOLUTION INC.

PA (UNIV-) UNIV NEBRASKA MEDICAL CENT.

XX Lockridge O, Watkins JD, Hancock JD;

XX WPI; 2002-636633/68.

PT New human butyrylcholinesterase variant polypeptides, useful for treating  
PT cocaine-induced conditions.

PS Example 3; Fig 2; 150p; English.

CC The present invention relates to mutants of human butyrylcholinesterase.  
CC The enzymes have an increased cocaine hydrolysis activity and can be used  
CC for treating a cocaine-induced condition. The present sequence is a  
CC protein shown in the exemplification of the invention

XX Sequence 574 AA;

Query Match 99.5%; Score 3096; DB 5; Length 574;  
Best Local Similarity 99.8%; Pred. No. 4.4e-277;  
Matches 573; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 EDDIIITKNGKVRGMNLTVEGGVTAFGLGIPYAPPLGRLFRKKPQSLTKMSDINMNTK 60
   |||||
DB 1 EDDIIITKNGKVRGMNLTVEGGVTAFGLGIPYAPPLGRLFRKKPQSLTKMSDINMNTK 60
QY 61 YANSCCNIDQSPFPFGHSEMMNPTDLSBDCLYANWIPAPKPNATVLIWYGGGFOT 120
   |||||
DB 61 YANSCCNIDQSPFPFGHSEMMNPTDLSBDCLYANWIPAPKPNATVLIWYGGGFOT 120
QY 121 GTSSLHYVDGKFLARVERIVVSMNYRVGALGFALPBNPAGNMGFLPDQQLALQWVOK 180
   |||||
DB 121 GTSSLHYVDGKFLARVERIVVSMNYRVGALGFALPBNPAGNMGFLPDQQLALQWVOK 180
QY 181 NIAAFGKPKSVTLFGESAGASVSLHLSFGSHSLFTRAILQSGSFNAPAVTSLYEAR 240
   |||||
DB 181 NIAAFGKPKSVTLFGESAGASVSLHLSFGSHSLFTRAILQSGSFNAPAVTSLYEAR 240
QY 241 NRTLNLAQLTGCSRENETEIIKCLRNKDPQELILNEAFVVPYGTPLSVNFGPTVDGFLT 300
   |||||
DB 241 NRTLNLAQLTGCSRENETEIIKCLRNKDPQELILNEAFVVPYGTPLSVNFGPTVDGFLT 300
QY 301 DMPDILLELGOQFKTQILVGNKDEGTWFLVYGAPGFSKDNNSIITRKEFOEGKIFPPG 360
   |||||
DB 301 DMPDILLELGOQFKTQILVGNKDEGTWFLVYGAPGFSKDNNSIITRKEFOEGKIFPPG 360
QY 361 VSEFGKESILFHYTDWVDORPENYREALGDVVDYNFICPALFTKFSWGNNAFFYY 420
   |||||
DB 361 VSEFGKESILFHYTDWVDORPENYREALGDVVDYNFICPALFTKFSWGNNAFFYY 420
QY 421 FEHRSSKLPWPBMWGVHGYEIEFVFGPLERRDNTYKAEELISRSIVKRWANFAKYNP 480
   |||||
DB 421 FEHRSSKLPWPBMWGVHGYEIEFVFGPLERRDNTYKAEELISRSIVKRWANFAKYNP 480
QY 481 NETONNSTSWPVFKSTEQKYLTLNTESTRIMTKLRAOCCRFWTSFPKYLEMTGNIDEAE 540
   |||||
DB 481 NETONNSTSWPVFKSTEQKYLTLNTESTRIMTKLRAOCCRFWTSFPKYLEMTGNIDEAE 540
QY 541 MEMKAGFHRNNNYMDMKQFNDYTSKESCVGL 574
   |||||
DB 541 MEMKAGFHRNNNYMDMKQFNDYTSKESCVGL 574

```

# RESULT 14

ABR62391 standard; protein; 574 AA.

```

XX ABR62391
XX ID ABR62391
XX AC ABR62391;
XX DT 03-OCT-2003 (first entry)
XX

```

DE Human butyrylcholinesterase.  
XX Human; butyrylcholinesterase; transgenic; poisoning; antidote; enzyme;  
KM EC-3.1.1.8.  
XX Homo sapiens.  
PN MO2003054182-A2.  
XX  
PD 03-JUL-2003.  
XX  
PF 19-DEC-2002; 2002W0-IB005526.  
XX  
PR 21-DEC-2001; 2001US-0344295P.  
XX  
PA (NEXT-) NEXIA BIOTECHNOLOGIES INC.  
PI Karatzas C, Huang Y, Lazaris A;  
XX  
DR WPI; 2003-559148/52.  
XX  
DR N-PDB; ACC64169.  
XX  
PT New transgenic mammal (e.g. goat) expressing a butyrylcholinesterase  
PT (BChE) enzyme in its milk or urine, useful for large-scale production of  
PT recombinant BChE to prevent or treat organophosphate poisoning or cocaine  
PT intoxication.  
XX  
PS Claim 10; Page 100-102; 112pp; English.  
XX  
CC The present sequence is the protein sequence of human  
CC butyrylcholinesterase (BChE). The invention provides methods for large-  
CC scale production of recombinant BChE in cell culture, and in the milk  
CC and/or urine of transgenic mammals. The genome of the transgenic mammal  
CC (e.g. goat) comprises a DNA sequence that encodes BChE operably linked to  
CC a mammary gland-specific promoter or to a urinary endothelium-specific  
CC promoter, and a signal sequence that provides secretion of the BChE  
CC enzyme into the milk or urine of the mammal. The recombinant BChE can be  
CC used in preventing and/or treating organophosphate pesticide poisoning,  
CC nerve gas poisoning, cocaine intoxication or succinylcholine-induced  
CC apnoea  
XX  
SQ Sequence 574 AA;  
XX  
Query Match 99.5%; Score 3096; DB 6; Length 574;  
Best Local Similarity 99.8%; Pred. No. 4.4e-277;  
Matches 573; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 EDDIIATKNGKVRGMNLTVFGGTVAFLGIPYAOPPLGLRFRKKQSLTKMSDINWATK 60  
DB 1 EDDIIATKNGKVRGMNLTVFGGTVAFLGIPYAOPPLGLRFRKKQSLTKMSDINWATK 60  
QY 61 YANSCCNINQSPFGFSGEMWNPNTLSDCLYLANWIPAPKXKATVLIWYGSGFOT 120  
DB 61 YANSCCNINQSPFGFSGEMWNPNTLSDCLYLANWIPAPKXKATVLIWYGSGFOT 120  
QY 121 GTSSLHYVDKFLARVERVIVSNVYRGALGFALPGNPEAPGNMGLPQQLALQWOK 180  
DB 121 GTSSLHYVDKFLARVERVIVSNVYRGALGFALPGNPEAPGNMGLPQQLALQWOK 180  
QY 181 NIAAFGNGNPKSVTLFGESAGAAVSILHLSPGSHSLFTRAILQSGSFNAFWAVTSLEYAR 240  
DB 181 NIAAFGNGNPKSVTLFGESAGAAVSILHLSPGSHSLFTRAILQSGSFNAFWAVTSLEYAR 240  
QY 241 NRTLNLAKLTGCSRENTETIICLRNDPOEILINAEFVVPYGPPLSVNGPTVDGFLT 300  
DB 241 NRTLNLAKLTGCSRENTETIICLRNDPOEILINAEFVVPYGPPLSVNGPTVDGFLT 300  
QY 301 DMEDILLETGOFKKTQILVGNKDEGTWPLVYGAPGSKNNSTIITRKEOEGKIFPPG 360  
DB 301 DMEDILLETGOFKKTQILVGNKDEGTWPLVYGAPGSKNNSTIITRKEOEGKIFPPG 360  
QY 361 VSEFGKESILFHYTDWVDORPENYRBAIDVVDYVFCPALEFTTKFSWGNNAFFYY 420  
DB 361 VSEFGKESILFHYTDWVDORPENYRBAIDVVDYVFCPALEFTTKFSWGNNAFFYY 420

DB 361 VSEFGKESILFHYTDWVDORPENYRBAIDVVDYVFCPALEFTTKFSWGNNAFFYY 420  
QY 421 FEHRSSKLPWEMWGMVGHGIEFVGLPLERRDNTKAEILSRIVKRWANPAKXGNP 480  
DB 421 FEHRSSKLPWEMWGMVGHGIEFVGLPLERRDNTKAEILSRIVKRWANPAKXGNP 480  
QY 481 NETQNNSTWVPVKSTEQKYLTLNTESTRIIMTKLRQOQCFWTSFPFKVLEMTGNIDEAR 540  
DB 481 NETQNNSTWVPVKSTEQKYLTLNTESTRIIMTKLRQOQCFWTSFPFKVLEMTGNIDEAR 540  
QY 541 MEWKAGFHRWNNYMDMKNOFNDYTSKESCVGL 574  
DB 541 MEWKAGFHRWNNYMDMKNOFNDYTSKESCVGL 574  
RESULT 15  
ID AEM00695 standard; protein; 574 AA.  
XX  
AC AEM00695;  
XX  
DT 15-JAN-2004 (first entry)  
XX  
XX Human butyrylcholinesterase protein.  
DE Human butyrylcholinesterase protein.  
XX  
KM Human; butyrylcholinesterase; enzyme.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Region 68..82  
FT /note="Region used to generate focused libraries of  
FT butyrylcholinesterase"  
FT Active-site 82  
FT Region 110..121  
FT /note="Region used to generate focused libraries of  
FT butyrylcholinesterase variants"  
FT Active-site 112  
FT Region 128  
FT Active-site 128  
FT Region 194..201  
FT /note="Region used to generate focused libraries of  
FT butyrylcholinesterase"  
FT Region 224..234  
FT /note="Region used to generate focused libraries of  
FT butyrylcholinesterase variants"  
FT Active-site 231  
FT Region 277..289  
FT /note="Region used to generate focused libraries of  
FT butyrylcholinesterase variants"  
FT Active-site 329  
FT Region 332  
FT Active-site 332  
FT Region 429..442  
FT /note="Region used to generate focused libraries of  
FT butyrylcholinesterase variants"  
FT Active-site 430  
FT Active-site 440  
XX  
PN US2003096401-A1.  
XX  
PD 22-MAY-2003.  
XX  
PF 28-NOV-2001; 2001US-00997209.  
XX  
PR 28-NOV-2000; 2000US-0367370P.  
XX  
PA (HUSE/) HUSE W D.  
XX  
PI Huse WD;  
XX  
DR WPI; 2003-786991/74.

XX Cell composition comprises non-yeast eukaryotic cells having diverse  
PT population of variant nucleic acids or heterologous nucleic acid  
PT fragments, useful for identifying polypeptide with optimized activity.

XX Example 11; Fig 8; Opp; English.

XX The invention relates to a cell composition comprising a population of  
CC non-yeast eukaryotic cells containing diverse population of variant  
CC nucleic acids, or heterologous nucleic acid fragments with distinct  
CC species of nucleic acid fragments, where each of the variant nucleic  
CC acids or heterologous nucleic acid fragments are expressed in different  
CC cell and located within each cell at an identical site in the genome. The  
CC invention is useful for identifying polypeptide with optimized activity  
CC and for identifying a polypeptide receptor for a ligand. The present  
CC sequence is human butyrylcholinesterase protein. This sequence is used in  
CC the exemplification of the invention

XX Sequence 574 AA;

Query Match 99.5%; Score 3096; DB 7; Length 574;

Best Local Similarity 99.8%; Pred. No. 4.4e-277;  
Matches 573; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 EDDIIATKNGKVRGMNLTVPFGTVAFLGIPYAPPLRLRFPKPSLTKMSDIMNATK 60
DB 1 EDDIIATKNGKVRGMNLTVPFGTVAFLGIPYAPPLRLRFPKPSLTKMSDIMNATK 60
QY 61 YANSCCNIDOSPFGHSEMMNPNTDLSBDCLYLWMIWIPAPKRNATVLIWYGGGFQT 120
DB 61 YANSCCNIDOSPFGHSEMMNPNTDLSBDCLYLWMIWIPAPKRNATVLIWYGGGFQT 120
QY 121 GTSSLHAYDGFKLARVERIVVSMNRYVAGLGFALPBNPAPGNMGLFDQALALQWVOK 180
DB 121 GTSSLHAYDGFKLARVERIVVSMNRYVAGLGFALPBNPAPGNMGLFDQALALQWVOK 180
QY 121 GTSSLHAYDGFKLARVERIVVSMNRYVAGLGFALPBNPAPGNMGLFDQALALQWVOK 180
DB 121 GTSSLHAYDGFKLARVERIVVSMNRYVAGLGFALPBNPAPGNMGLFDQALALQWVOK 180
QY 181 NIAAFGNPKSVTLFGESAGAASVSLHLSPGSHSLFTRAILLOGSFNAPWATVSLYEAR 240
DB 181 NIAAFGNPKSVTLFGESAGAASVSLHLSPGSHSLFTRAILLOGSFNAPWATVSLYEAR 240
QY 181 NIAAFGNPKSVTLFGESAGAASVSLHLSPGSHSLFTRAILLOGSFNAPWATVSLYEAR 240
DB 181 NIAAFGNPKSVTLFGESAGAASVSLHLSPGSHSLFTRAILLOGSFNAPWATVSLYEAR 240
QY 241 NRTLNIAKLTCGSRNETEIIKCLRNKDPQETILLNEAFVVPYGTPLSVNFGPTVDGFLT 300
DB 241 NRTLNIAKLTCGSRNETEIIKCLRNKDPQETILLNEAFVVPYGTPLSVNFGPTVDGFLT 300
QY 241 NRTLNIAKLTCGSRNETEIIKCLRNKDPQETILLNEAFVVPYGTPLSVNFGPTVDGFLT 300
DB 241 NRTLNIAKLTCGSRNETEIIKCLRNKDPQETILLNEAFVVPYGTPLSVNFGPTVDGFLT 300
QY 301 DMPDILLEGQFKTKQIILVGNKDEGTWFLVYGAFGSKNNNSITTRKEPQGLKIFPPG 360
DB 301 DMPDILLEGQFKTKQIILVGNKDEGTWFLVYGAFGSKNNNSITTRKEPQGLKIFPPG 360
QY 301 DMPDILLEGQFKTKQIILVGNKDEGTWFLVYGAFGSKNNNSITTRKEPQGLKIFPPG 360
DB 301 DMPDILLEGQFKTKQIILVGNKDEGTWFLVYGAFGSKNNNSITTRKEPQGLKIFPPG 360
QY 361 VSEFGKESILFHYTDVDDQRPENYREALGVGVDFNFCPALBETKKESEWGNNAFFY 420
DB 361 VSEFGKESILFHYTDVDDQRPENYREALGVGVDFNFCPALBETKKESEWGNNAFFY 420
QY 421 FEHRSKSLPMPWEMGVAGYEIEFVGLPDERDNTYKAEILSRISYKRNANFKYGNP 480
DB 421 FEHRSKSLPMPWEMGVAGYEIEFVGLPDERDNTYKAEILSRISYKRNANFKYGNP 480
QY 421 FEHRSKSLPMPWEMGVAGYEIEFVGLPDERDNTYKAEILSRISYKRNANFKYGNP 480
DB 421 FEHRSKSLPMPWEMGVAGYEIEFVGLPDERDNTYKAEILSRISYKRNANFKYGNP 480
QY 481 NETQNNSTSWPVKSTEQKYLTLNTESTRIMTKLRNQOCCRFWTSFPFKLEMTGNIDAE 540
DB 481 NETQNNSTSWPVKSTEQKYLTLNTESTRIMTKLRNQOCCRFWTSFPFKLEMTGNIDAE 540
QY 541 WEWKAGFHRNNNTMMDMKQNFNDYTSKESCVGL 574
DB 541 WEWKAGFHRNNNTMMDMKQNFNDYTSKESCVGL 574

```

RESULT 16

ADP44639 standard; protein; 574 AA.

ADP44639;

09-SEP-2004 (first entry)

XX

DE Human butyrylcholinesterase wild-type protein.

XX butyrylcholinesterase, cytosolic; metastatic colorectal cancer; ovarian;  
KM lung; non-Hodgkin's lymphoma; gene therapy; human; wild-type; enzyme.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Disulfide-bond 65..92

FT Disulfide-bond 252..263

FT Disulfide-bond 400..519

FT Disulfide-bond /label = Disulphide\_bond

FT Disulfide-bond /label = Disulphide\_bond

FT Disulfide-bond /label = Disulphide\_bond

FT Disulfide-bond /label = Disulphide\_bond

FT Disulfide-bond /label = Disulphide\_bond

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FT Disulfide-bond /label = Disulphide\_bond



Db 301 DMDIILLEGQFKKTQLLVGNKDEGTAFVYGAPGFSKDNNSIITRKEFOEGLKIFPPG 360  
QY 361 VSEFGKESILFHTYDWDQDQRPENYREALGDVGDVNFICPALBFTKKFSMGNNAFFYY 420  
Db 361 VSEFGKESILFHTYDWDQDQRPENYREALGDVGDVNFICPALBFTKKFSMGNNAFFYY 420  
QY 421 FEHRSSKLPWPMWGVHGYEIEFVFGPLERDNYTKAEIILSRSIYKMANPAKYGNP 480  
Db 421 FEHRSSKLPWPMWGVHGYEIEFVFGPLERDNYTKAEIILSRSIYKMANPAKYGNP 480  
QY 481 NETQNNSTSWPVFKSTQKYLTLNTESTRIMTKLRAQOCRFWTSFPFKVLEMTGNIDAE 540  
Db 481 NETQNNSTSWPVFKSTQKYLTLNTESTRIMTKLRAQOCRFWTSFPFKVLEMTGNIDAE 540  
QY 541 MEWKAGFHRMNNYMMQKQFNQDYSKESCVGL 574  
Db 541 MEWKAGFHRMNNYMMQKQFNQDYSKESCVGL 574

RESULT 17  
ADRO1077  
ID ADRO1077 standard; protein; 574 AA.  
AC ADRO1077;  
XX 23-SEP-2004 (first entry)  
DT XX  
DE Human butyrylcholinesterase.  
KM butyrylcholinesterase; cocaine-induced condition;  
KW cocaine-based butyrylcholinesterase substrate; cocaine-overdose;  
KM cocaine addiction; human; butyrylcholinesterase variant.  
OS Homo sapiens.  
XX US2004121970-A1.  
PN 24-JUN-2004.  
PD 20-DEC-2002; 2002US-00324466.  
PF 20-DEC-2002; 2002US-00324466.  
XX 20-DEC-2002; 2002US-00324466.  
PR 20-DEC-2002; 2002US-00324466.  
PA (WATK/) WATKINS J D.  
PA (PANC/) PANCOCK J D.  
PI Watkins JD, Pancok JD;  
XX WPI; 2004-468195/44.  
DR N-PSDB; ADRO1076.  
PT New butyrylcholinesterase variant polypeptide, useful in treating cocaine  
PT -induced condition, i.e. cocaine-overdose or cocaine addiction.  
XX  
XX Disclosure; SEQ ID NO 44; 131bp; English.  
PS  
XX The invention describes a butyrylcholinesterase variant polypeptide (I)  
CC comprising any of the 21 sequences of 57 amino acids each (EVEN SEQ ID  
CC NOS: 2-42) or their functional fragments. Also described are: a nucleic  
CC acid encoding (I) comprising any of the 21 nucleic acid sequences of 2416  
CC bp each (ODD SEQ ID NOS: 1-41) or their fragments; a method of treating a  
CC cocaine-induced condition; and a method of hydrolysing a cocaine-based  
CC butyrylcholinesterase substrate. (I) is butyrylcholinesterase variant  
CC polypeptide comprising any of the 21 sequences of 57 amino acids each  
CC (EVEN SEQ ID NOS: 2-42), encoded by a nucleic acid comprising any of the  
CC 21 nucleic acid sequences of 2416 bp each (ODD SEQ ID NOS: 1-41). The  
CC butyrylcholinesterase variant polypeptides and nucleic acids and methods  
CC are useful in treating cocaine-induced condition i.e. cocaine-overdose or  
CC cocaine addiction. This is the amino acid sequence of human  
CC butyrylcholinesterase.  
XX  
XX Sequence 574 AA;  
SQ

Query Match 99.5%; Score 3096; DB 8; Length 574;  
Best Local Similarity 99.8%; Pred. No. 4,4e-277;  
Matches 573; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 EDDIIITKKGKRGMLTVPGGVTAFLGIPAPQPLGLRFKKPQSLTKMSDINWATK 60  
Db 1 EDDIIITKKGKRGMLTVPGGVTAFLGIPAPQPLGLRFKKPQSLTKMSDINWATK 60  
QY 61 YANSCCNIDQSPFGFSGEMMNPNTDLSBDCYLANWIMAPKKNATVIMWGGGFGQT 120  
Db 61 YANSCCNIDQSPFGFSGEMMNPNTDLSBDCYLANWIMAPKKNATVIMWGGGFGQT 120  
QY 121 GTSSLHYDQKFLARVERVIVSMNRYVAGLGFALPGNPBAPGNMGLPQOALQWVOK 180  
Db 121 GTSSLHYDQKFLARVERVIVSMNRYVAGLGFALPGNPBAPGNMGLPQOALQWVOK 180  
QY 181 NIAAFGNPNSVTLFGSSAGAAVSLLHLPSSLSLFTRAIILQSGSPNAAPAVTSLYEAR 240  
Db 181 NIAAFGNPNSVTLFGSSAGAAVSLLHLPSSLSLFTRAIILQSGSPNAAPAVTSLYEAR 240  
QY 241 NRTLNIAKLTCGSRNETEIIKCLRNKDPQOILNLEAFVVPYGTPLSVNFGPTVDGDFLT 300  
Db 241 NRTLNIAKLTCGSRNETEIIKCLRNKDPQOILNLEAFVVPYGTPLSVNFGPTVDGDFLT 300  
QY 301 DMDIILLEGQFKKTQLLVGNKDEGTAFVYGAPGFSKDNNSIITRKEFOEGLKIFPPG 360  
Db 301 DMDIILLEGQFKKTQLLVGNKDEGTAFVYGAPGFSKDNNSIITRKEFOEGLKIFPPG 360  
QY 361 VSEFGKESILFHTYDWDQDQRPENYREALGDVGDVNFICPALBFTKKFSMGNNAFFYY 420  
Db 361 VSEFGKESILFHTYDWDQDQRPENYREALGDVGDVNFICPALBFTKKFSMGNNAFFYY 420  
QY 421 FEHRSSKLPWPMWGVHGYEIEFVFGPLERDNYTKAEIILSRSIYKMANPAKYGNP 480  
Db 421 FEHRSSKLPWPMWGVHGYEIEFVFGPLERDNYTKAEIILSRSIYKMANPAKYGNP 480  
QY 481 NETQNNSTSWPVFKSTQKYLTLNTESTRIMTKLRAQOCRFWTSFPFKVLEMTGNIDAE 540  
Db 481 NETQNNSTSWPVFKSTQKYLTLNTESTRIMTKLRAQOCRFWTSFPFKVLEMTGNIDAE 540  
QY 541 MEWKAGFHRMNNYMMQKQFNQDYSKESCVGL 574  
Db 541 MEWKAGFHRMNNYMMQKQFNQDYSKESCVGL 574

RESULT 18  
AA59235  
ID AA59235 standard; protein; 602 AA.  
AC AA59235;  
XX 27-MAR-2000 (first entry)  
DT XX  
DE Human butyryl cholinesterase (BuChE) mutant.  
XX  
XX Organophosphate; detoxification; esterase; acetylcholinesterase; AChE;  
KM butyrylcholinesterase; BuChE; carboxylesterase; CnE; sheep dip; human;  
KM nerve agent; organophosphorus acid anhydride; OPA; mutant.  
XX  
XX Homo sapiens.  
OS Synthetic.  
XX US6001625-A.  
PN 14-DEC-1999.  
PD 19-MAY-1995; 95US-00446100.  
XX 19-MAY-1995; 95US-00446100.  
PP 19-MAY-1995; 95US-00446100.  
XX (USSA ) US SEC OF ARMY.  
PA Broomfield CA, Lockridge O, Millard CB;  
XX  
XX  
PI

XX MPI, 2000-096137/08.

XX Enhancing the organophosphate detoxifying capabilities of esterases for  
PT the treatment of organophosphate poisoning.

XX Disclosure; Col 99-102; 64pp; English.

XX The invention provides a method of enhancing organophosphate detoxifying  
CC capabilities of esterases (either human acetylcholinesterases (AChE),  
CC human butyrylcholinesterases (BuChE) and/or carboxylesterases (CAE)), that  
CC comprises substituting a histidine residue for 1 or more amino acid(s)  
CC within 6 Angstrom of an active site serine. The method may be used for  
CC enhancing organophosphate detoxifying capabilities of esterases (either  
CC human AChE, human BuChE and/or human CAE). The modified esterases may  
CC then be used to treat agricultural workers poisoned with organophosphates  
CC through contact with chemical such as sheep dips. They may also be used  
CC to treat military personnel contaminated by chemical weaponry such as  
CC nerve agents. Additionally, the esterases may also be used to  
CC decontaminate ground and buildings and equipment used to store, or  
CC contaminated by organophosphates. The method produces esterases with  
CC improved detoxification properties over naturally occurring  
CC organophosphorus acid anhydride (OPAA) hydrolyzing enzymes. They are also  
CC less likely to be inactivated by the OPAA

XX Sequence 602 AA;

Query Match 99.5%; Score 3096; DB 3; Length 602;

Best Local Similarity 99.8%; Pred. No. 4.7e-277;  
Matches 573; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

1 EDDIIATKNGKVRGMNLTVEGVTAFGLIPYAPPLGRKFKKPKQSLTKMSDINWATK 60
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61 YANSCCONIDQSPFGFSGEMNPNNTDLSBDCLYLNVWIPAPKPKNAATVLIWYGGGFQT 120
89 YANSCCONIDQSPFGFSGEMNPNNTDLSBDCLYLNVWIPAPKPKNAATVLIWYGGGFQT 148
121 GTSSLIHYVDGKFLARVERVIVSMNRYVAGLFGFLALPGNPEAPGNMGLFDQQLALQWQK 180
149 GTSSLIHYVDGKFLARVERVIVSMNRYVAGLFGFLALPGNPEAPGNMGLFDQQLALQWQK 208
181 NIAAFGNGKSVTLFGESAGAAVSILHLSPGSHSLFTRAILQSGSFNAPMAVTSIYEAR 240
209 NIAAFGNGKSVTLFGESAGAAVSILHLSPGSHSLFTRAILQSGSFNAPMAVTSIYEAR 268
241 NRTIANLAKITGCSRENTEIILKLRNKDQOEILLNEAFVVPYGTPLSVNFGPTVDGDFLT 300
269 NRTIANLAKITGCSRENTEIILKLRNKDQOEILLNEAFVVPYGTPLSVNFGPTVDGDFLT 328
301 DMPDILLEGQFKKTOIIVGNKDECTWFLVVGAPGFSKDNNSITTRKEFGGLKIFPPG 360
329 DMPDILLEGQFKKTOIIVGNKDECTWFLVVGAPGFSKDNNSITTRKEFGGLKIFPPG 388
361 VSEFGKESILFHTYDWDDORPENYREALGVVDVNFICPALFEFKKSEWGNNAFFY 420
389 VSEFGKESILFHTYDWDDORPENYREALGVVDVNFICPALFEFKKSEWGNNAFFY 448
421 FEHRSKLPWPEWNGVNGHGEIEFVGLPLERDNTTKABELLSRIVRMANFAKYGP 480
449 FEHRSKLPWPEWNGVNGHGEIEFVGLPLERDNTTKABELLSRIVRMANFAKYGP 508
481 NETONNSTSWPVPESTEOKTLTNTSESTRIMTKLRAOQCFMTSPFKVLEMTGNIDEAE 540
509 NETONNSTSWPVPESTEOKTLTNTSESTRIMTKLRAOQCFMTSPFKVLEMTGNIDEAE 568
541 WEMKAGFRMNNYMMQWNOFNDYTSKESCVGL 574
569 WEMKAGFRMNNYMMQWNOFNDYTSKESCVGL 602

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AA949471  
ID AA949471 standard; protein; 602 AA.

XX AA949471;

XX 27-MAR-2000 (first entry)

XX Human wild-type butyryl cholinesterase (BuChE).

XX Organophosphate; detoxification; esterase; acetylcholinesterase; AChE;  
XX butyrylcholinesterase; BuChE; carboxylesterase; CAE; sheep dip; human;  
XX nerve agent; organophosphorus acid anhydride; OPAA.

XX Homo sapiens.

XX US6001625-A.

XX 14-DEC-1999.

XX 19-MAY-1995; 95US-00446100.

XX 19-MAY-1995; 95US-00446100.

XX (USSA ) US SEC OF ARMY.

XX Broomfield CA, Lockridge O, Millard CB;

XX MPI, 2000-096137/08.

XX Enhancing the organophosphate detoxifying capabilities of esterases for  
PT the treatment of organophosphate poisoning.

XX Disclosure; Col 3-4; 64pp; English.

XX The invention provides a method of enhancing organophosphate detoxifying  
CC capabilities of esterases (either human acetylcholinesterases (AChE),  
CC human butyrylcholinesterases (BuChE) and/or carboxylesterases (CAE)), that  
CC comprises substituting a histidine residue for 1 or more amino acid(s)  
CC within 6 Angstrom of an active site serine. The method may be used for  
CC enhancing organophosphate detoxifying capabilities of esterases (either  
CC human AChE, human BuChE and/or human CAE). The modified esterases may  
CC then be used to treat agricultural workers poisoned with organophosphates  
CC through contact with chemical such as sheep dips. They may also be used  
CC to treat military personnel contaminated by chemical weaponry such as  
CC nerve agents. Additionally, the esterases may also be used to  
CC decontaminate ground and buildings and equipment used to store, or  
CC contaminated by organophosphates. The method produces esterases with  
CC improved detoxification properties over naturally occurring  
CC organophosphorus acid anhydride (OPAA) hydrolyzing enzymes. They are also  
CC less likely to be inactivated by the OPAA

XX Sequence 602 AA;

Query Match 99.5%; Score 3096; DB 3; Length 602;

Best Local Similarity 99.8%; Pred. No. 4.7e-277;  
Matches 573; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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1 EDDIIATKNGKVRGMNLTVEGVTAFGLIPYAPPLGRKFKKPKQSLTKMSDINWATK 60
29 EDDIIATKNGKVRGMNLTVEGVTAFGLIPYAPPLGRKFKKPKQSLTKMSDINWATK 88
61 YANSCCONIDQSPFGFSGEMNPNNTDLSBDCLYLNVWIPAPKPKNAATVLIWYGGGFQT 120
89 YANSCCONIDQSPFGFSGEMNPNNTDLSBDCLYLNVWIPAPKPKNAATVLIWYGGGFQT 148
121 GTSSLIHYVDGKFLARVERVIVSMNRYVAGLFGFLALPGNPEAPGNMGLFDQQLALQWQK 180
149 GTSSLIHYVDGKFLARVERVIVSMNRYVAGLFGFLALPGNPEAPGNMGLFDQQLALQWQK 208
181 NIAAFGNGKSVTLFGESAGAAVSILHLSPGSHSLFTRAILQSGSFNAPMAVTSIYEAR 240
209 NIAAFGNGKSVTLFGESAGAAVSILHLSPGSHSLFTRAILQSGSFNAPMAVTSIYEAR 268

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QY 241 NRTLNIAKLTCGSRNETEIIKCLRNDPOEIIINAEFVVPYGTPLSVNGPTVDGDFLT 300  
 DB 269 NRTLNIAKLTCGSRNETEIIKCLRNDPOEIIINAEFVVPYGTPLSVNGPTVDGDFLT 328  
 QY 301 DMPDILLELQPKKTOILVGNKDEGTWFLVYGAPGSKNNSTITRKEPBGKIFPPG 360  
 DB 329 DMPDILLELQPKKTOILVGNKDEGTWFLVYGAPGSKNNSTITRKEPBGKIFPPG 388  
 QY 361 VSEFGKESILFHYTDWDDORPENYREALGDVVDYNYFCPALFETKKSFWMGNAFFYY 420  
 DB 389 VSEFGKESILFHYTDWDDORPENYREALGDVVDYNYFCPALFETKKSFWMGNAFFYY 448  
 QY 421 FEHRSSTLPPPEWVGWVGIEIEFVGLPLERRDNYTKAEIISRSIVKRWANPAKYGNP 480  
 DB 449 FEHRSSTLPPPEWVGWVGIEIEFVGLPLERRDNYTKAEIISRSIVKRWANPAKYGNP 508  
 QY 481 NETONNSTSWPVFSTOKYLTINTESTRIMTKLRAQOCRFWTSFPFKVLEMTGNIDBAE 540  
 DB 509 NETONNSTSWPVFSTOKYLTINTESTRIMTKLRAQOCRFWTSFPFKVLEMTGNIDBAE 568  
 QY 541 MEWKAGFHRNNNTYMDWKQNFNDYTSKKESCVGL 574  
 DB 569 MEWKAGFHRNNNTYMDWKQNFNDYTSKKESCVGL 602

RESULT 20

AAV44573 ID AAV44573 standard; protein; 602 AA.

XX AAV44573;

XX 04-APR-2000 (first entry)

XX Human wild type Butyrylcholinesterase (BChE) protein.

XX Butyrylcholinesterase; BChE allele; neurological disease; treatment;  
 KW therapy; allelic variant; BChE-K; apoE4 allele; neurofibromatosis;  
 KM non-AD neurologic disease; Alzheimer's disease; Huntington's disease;  
 KM depression; amyotrophic lateral sclerosis; multiple sclerosis; stroke;  
 KM Parkinson's disease; multi-infarct dementia; human.

XX Homo sapiens.

XX WO966072-A2.

XX 23-DEC-1999.

XX 16-JUN-1999; 99WO-IB001298.

XX 16-JUN-1998; 98US-0089406P.

XX (NOVA-) NOVA MOLECULAR INC.

XX Sevigny P, Wiebusch H, Schapbert K,

XX WPI; 2000-126550/11.

XX N-PSDB; AA249470.

XX Prediction of drug efficacy for treating neurological diseases like

XX Alzheimer's disease, neurofibromatosis, Huntington's disease.

XX Example 1; Fig 3; 37pp; English.

XX The present sequence is the wild type human butyrylcholinesterase (BChE)  
 CC protein. Determining BChE allele status of a patient helps predicting  
 CC risk for neurologic diseases, efficacy of therapy and determining  
 CC treatment protocol. Presence of BChE allelic variant, BChE-K and apoE4  
 CC allele indicate patient's risk for having a neurological disease. This  
 CC method enables treating Alzheimer's disease, depression,  
 CC neurofibromatosis, Huntington's disease, amyotrophic lateral sclerosis,  
 CC multiple sclerosis, stroke, Parkinson's disease, multi-infarct dementia  
 CC and other non-AD neurological diseases

SQ Sequence 602 AA;

Query Match 99.5%; Score 3096; DB 3; Length 602;  
 Best Local Similarity 99.8%; Pred. No. 4,7e-277;  
 Matches 573; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDDIIATKNGKVRGNMLTVFGGTVAFLGIPYAQPELGLRFEKKPQSLTKMSDIWATK 60  
 DB 29 EDDIIATKNGKVRGNMLTVFGGTVAFLGIPYAQPELGLRFEKKPQSLTKMSDIWATK 88  
 QY 61 YANSCCNIDIOSPPGFGSEMNPNNDLSBDCLYLWNTIAPKPKATVLIWYGGSPQT 120  
 DB 89 YANSCCNIDIOSPPGFGSEMNPNNDLSBDCLYLWNTIAPKPKATVLIWYGGSPQT 148  
 QY 121 GTSLSHYDQKFLARVVRVIVSMNRYVAGLGFALPGNBEAPGNMGLFQOQLALQVOK 180  
 DB 149 GTSLSHYDQKFLARVVRVIVSMNRYVAGLGFALPGNBEAPGNMGLFQOQLALQVOK 208  
 QY 181 NIAAFGNPKSVTLFGESAGAASVSLHLSPGSHSLFTRAILOSGSFNAPMAVTSLEYAR 240  
 DB 209 NIAAFGNPKSVTLFGESAGAASVSLHLSPGSHSLFTRAILOSGSFNAPMAVTSLEYAR 268  
 QY 241 NRTLNIAKLTCGSRNETEIIKCLRNDPOEIIINAEFVVPYGTPLSVNGPTVDGDFLT 300  
 DB 269 NRTLNIAKLTCGSRNETEIIKCLRNDPOEIIINAEFVVPYGTPLSVNGPTVDGDFLT 328  
 QY 301 DMPDILLELQPKKTOILVGNKDEGTWFLVYGAPGSKNNSTITRKEPBGKIFPPG 360  
 DB 329 DMPDILLELQPKKTOILVGNKDEGTWFLVYGAPGSKNNSTITRKEPBGKIFPPG 388  
 QY 361 VSEFGKESILFHYTDWDDORPENYREALGDVVDYNYFCPALFETKKSFWMGNAFFYY 420  
 DB 389 VSEFGKESILFHYTDWDDORPENYREALGDVVDYNYFCPALFETKKSFWMGNAFFYY 448  
 QY 421 FEHRSSTLPPPEWVGWVGIEIEFVGLPLERRDNYTKAEIISRSIVKRWANPAKYGNP 480  
 DB 449 FEHRSSTLPPPEWVGWVGIEIEFVGLPLERRDNYTKAEIISRSIVKRWANPAKYGNP 508  
 QY 481 NETONNSTSWPVFSTOKYLTINTESTRIMTKLRAQOCRFWTSFPFKVLEMTGNIDBAE 540  
 DB 509 NETONNSTSWPVFSTOKYLTINTESTRIMTKLRAQOCRFWTSFPFKVLEMTGNIDBAE 568  
 QY 541 MEWKAGFHRNNNTYMDWKQNFNDYTSKKESCVGL 574  
 DB 569 MEWKAGFHRNNNTYMDWKQNFNDYTSKKESCVGL 602

RESULT 21

ABR62392 ID ABR62392 standard; protein; 602 AA.

XX ABR62392;

XX 03-OCT-2003 (first entry)

XX Human butyrylcholinesterase.

XX Human; butyrylcholinesterase; transgenic; poisoning; antidote; enzyme;

XX EC-3.1.1.8.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Peptide 1..18 /label= signal peptide

XX Protein 19..602 /label= Butyrylcholinesterase

XX WO2003054182-A2.

XX 03-JUL-2003.

XX 19-DEC-2002; 2002WO-IB005526.

XX 21-DEC-2001; 2001US-0344295P.  
XX (NEXT-) NEXIA BIOTECHNOLOGIES INC.  
XX Karatzas C, Huang Y, Lazaris A;  
XX WPI; 2003-559148/52.  
XX N-PSDB; ACC64170.  
XX  
XX New transgenic mammal (e.g. goat) expressing a butyrylcholinesterase  
XX (BChE) enzyme in its milk or urine, useful for large-scale production of  
XX recombinant BChE to prevent or treat organophosphate poisoning or cocaine  
XX intoxication.  
XX  
XX Disclosure; Fig 1A; 112pp; English.  
XX  
XX The present sequence is the protein sequence of human  
XX butyrylcholinesterase (BChE), including the native signal peptide which  
XX is cleaved during processing to produce the mature BChE protein. The  
XX invention provides methods for large-scale production of recombinant BChE  
XX in cell culture, and in the milk and/or urine of transgenic mammals. The  
XX genome of the transgenic mammal (e.g. goat) comprises a DNA sequence that  
XX encodes BChE operably linked to a mammary gland-specific promoter or to a  
XX urinary endothelium-specific promoter, and a signal sequence that  
XX provides secretion of the BChE enzyme into the milk or urine of the  
XX mammal. The recombinant BChE can be used in preventing and/or treating  
XX organophosphate pesticide poisoning, nerve gas poisoning, cocaine  
XX intoxication or succinylcholine-induced apnoea  
XX  
SQ Sequence 602 AA;  
Query Match 99.5%; Score 3096; DB 6; Length 602;  
Best Local Similarity 99.8%; Pred. No. 4.7e-277;  
Matches 573; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
XX  
QY 1 EDDIIITATKNGKRGKGNLTVFGGTVAFLGIPYAPPLGRKPKOSLTKMSDINWATK 60  
DB EDDIIITATKNGKRGKGNLTVFGGTVAFLGIPYAPPLGRKPKOSLTKMSDINWATK 88  
QY 61 YANSCCNIDQSPFGHSEMNPNNTDLSBDCLYLWVWIPAPKRNATVLIWYGGGFQT 120  
DB YANSCCNIDQSPFGHSEMNPNNTDLSBDCLYLWVWIPAPKRNATVLIWYGGGFQT 148  
QY 121 GTSSLHYDGGKFLARVERVIVSMNRYVAGLGFALPGNBPAPGNMGLPQQLALQWVOK 180  
DB GTSSLHYDGGKFLARVERVIVSMNRYVAGLGFALPGNBPAPGNMGLPQQLALQWVOK 208  
QY 149 GTSSLHYDGGKFLARVERVIVSMNRYVAGLGFALPGNBPAPGNMGLPQQLALQWVOK 208  
DB 149 GTSSLHYDGGKFLARVERVIVSMNRYVAGLGFALPGNBPAPGNMGLPQQLALQWVOK 208  
QY 181 NIAAFGNPKSVTLFGESAGAAVSLSLSPGSHSLFTRAILQSGSPNAPWATSLYEAR 240  
DB NIAAFGNPKSVTLFGESAGAAVSLSLSPGSHSLFTRAILQSGSPNAPWATSLYEAR 268  
QY 209 NIAAFGNPKSVTLFGESAGAAVSLSLSPGSHSLFTRAILQSGSPNAPWATSLYEAR 268  
DB 209 NIAAFGNPKSVTLFGESAGAAVSLSLSPGSHSLFTRAILQSGSPNAPWATSLYEAR 268  
QY 241 NRTNLAKLTGCGRENTEITIKLRNKPDEIILNEAFVVPYGTPLSVNFGPTVDGFLT 300  
DB NRTNLAKLTGCGRENTEITIKLRNKPDEIILNEAFVVPYGTPLSVNFGPTVDGFLT 328  
QY 269 NRTNLAKLTGCGRENTEITIKLRNKPDEIILNEAFVVPYGTPLSVNFGPTVDGFLT 328  
DB 269 NRTNLAKLTGCGRENTEITIKLRNKPDEIILNEAFVVPYGTPLSVNFGPTVDGFLT 328  
QY 301 DMPDILLELQGFKKTKQLLVGNKDEGTPFLVYAGPGSKNNSIITRKEFOEGSKITFPFG 360  
DB DMPDILLELQGFKKTKQLLVGNKDEGTPFLVYAGPGSKNNSIITRKEFOEGSKITFPFG 388  
QY 329 DMPDILLELQGFKKTKQLLVGNKDEGTPFLVYAGPGSKNNSIITRKEFOEGSKITFPFG 388  
DB 329 DMPDILLELQGFKKTKQLLVGNKDEGTPFLVYAGPGSKNNSIITRKEFOEGSKITFPFG 388  
QY 361 VSEBGEKSLIFHYTDWDDQRPENYREALGDVVDYNIICPALFTKKFSWGNNAFFYY 420  
DB VSEBGEKSLIFHYTDWDDQRPENYREALGDVVDYNIICPALFTKKFSWGNNAFFYY 448  
QY 389 VSEBGEKSLIFHYTDWDDQRPENYREALGDVVDYNIICPALFTKKFSWGNNAFFYY 448  
DB 389 VSEBGEKSLIFHYTDWDDQRPENYREALGDVVDYNIICPALFTKKFSWGNNAFFYY 448  
QY 421 FEHRSSKLPMPBEMGVHGEIEIEFVGLPLERRDNNTYKAEIILSRSLYKRNANPAKYNP 480  
DB FEHRSSKLPMPBEMGVHGEIEIEFVGLPLERRDNNTYKAEIILSRSLYKRNANPAKYNP 508  
QY 449 FEHRSSKLPMPBEMGVHGEIEIEFVGLPLERRDNNTYKAEIILSRSLYKRNANPAKYNP 508  
DB 449 FEHRSSKLPMPBEMGVHGEIEIEFVGLPLERRDNNTYKAEIILSRSLYKRNANPAKYNP 508  
QY 481 NETONNSWVPFSTQKYLTLNTESTRIWTKLRAOCCRFMTSPFPVLEMTGNIDBAE 540  
DB NETONNSWVPFSTQKYLTLNTESTRIWTKLRAOCCRFMTSPFPVLEMTGNIDBAE 568  
QY 509 NETONNSWVPFSTQKYLTLNTESTRIWTKLRAOCCRFMTSPFPVLEMTGNIDBAE 568  
DB 509 NETONNSWVPFSTQKYLTLNTESTRIWTKLRAOCCRFMTSPFPVLEMTGNIDBAE 568  
QY 541 WEMKAGFHRNNNMMDWKQNFNDYTSKESCVGL 574  
DB 541 WEMKAGFHRNNNMMDWKQNFNDYTSKESCVGL 574

DB 569 WEMKAGFHRNNNMMDWKQNFNDYTSKESCVGL 602  
|||||  
RESULT 22  
ADP90908  
ID ADF90908 standard; protein; 602 AA.  
XX  
XX ADF90908;  
AC  
XX 26-FEB-2004 (first entry)  
DT  
XX Human hepatic-fibrosis disease marker protein SEQ ID 370.  
DE  
XX Hepatic fibrosis; marker; chronic hepatitis; liver cirrhosis;  
KW hepatic carcinoma; human.  
XX  
XX Homo sapiens.  
OS  
XX JP2003259877-A.  
PN  
XX 16-SEP-2003.  
PD  
XX 11-MAR-2002; 2002JP-00065013.  
PF  
XX 11-MAR-2002; 2002JP-00065013.  
PR  
XX 11-MAR-2002; 2002JP-00065013.  
XX  
XX (SUMU ) SUMITOMO SEIYAKU KK.  
PA  
XX WPI; 2003-821598/77.  
DR  
XX  
XX Hepatic fibrosis disease markers comprising polynucleotides or  
XX antibodies, useful for improved diagnosis, screening and developing drugs  
XX to treat hepatitis, to control cirrhosis and carcinoma.  
PT  
XX  
XX Claim 3; SEQ ID NO 370; 313pp; Japanese.  
PS  
XX  
XX The present invention relates to hepatic-fibrosis disease markers  
XX (ADP90539-ADP90871) and related proteins (ADP90872-ADP90917). The  
XX sequences are useful for detecting and treating hepatic fibrosis caused  
XX by alcohol consumption, virus infection, etc., and the associated chronic  
XX hepatitis, etc. leading to liver cirrhosis and hepatic carcinoma. The  
XX markers allow the cause of hepatic fibrosis to be clarified (diagnostic  
XX precision), so more suitable treatments can be developed and given.  
XX  
SQ Sequence 602 AA;  
Query Match 99.5%; Score 3096; DB 7; Length 602;  
Best Local Similarity 99.8%; Pred. No. 4.7e-277;  
Matches 573; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
XX  
QY 1 EDDIIITATKNGKRGKGNLTVFGGTVAFLGIPYAPPLGRKPKOSLTKMSDINWATK 60  
DB EDDIIITATKNGKRGKGNLTVFGGTVAFLGIPYAPPLGRKPKOSLTKMSDINWATK 88  
QY 29 EDDIIITATKNGKRGKGNLTVFGGTVAFLGIPYAPPLGRKPKOSLTKMSDINWATK 88  
DB 29 EDDIIITATKNGKRGKGNLTVFGGTVAFLGIPYAPPLGRKPKOSLTKMSDINWATK 88  
QY 61 YANSCCNIDQSPFGHSEMNPNNTDLSBDCLYLWVWIPAPKRNATVLIWYGGGFQT 120  
DB YANSCCNIDQSPFGHSEMNPNNTDLSBDCLYLWVWIPAPKRNATVLIWYGGGFQT 148  
QY 89 YANSCCNIDQSPFGHSEMNPNNTDLSBDCLYLWVWIPAPKRNATVLIWYGGGFQT 148  
DB 89 YANSCCNIDQSPFGHSEMNPNNTDLSBDCLYLWVWIPAPKRNATVLIWYGGGFQT 148  
QY 121 GTSSLHYDGGKFLARVERVIVSMNRYVAGLGFALPGNBPAPGNMGLPQQLALQWVOK 180  
DB GTSSLHYDGGKFLARVERVIVSMNRYVAGLGFALPGNBPAPGNMGLPQQLALQWVOK 208  
QY 149 GTSSLHYDGGKFLARVERVIVSMNRYVAGLGFALPGNBPAPGNMGLPQQLALQWVOK 208  
DB 149 GTSSLHYDGGKFLARVERVIVSMNRYVAGLGFALPGNBPAPGNMGLPQQLALQWVOK 208  
QY 181 NIAAFGNPKSVTLFGESAGAAVSLSLSPGSHSLFTRAILQSGSPNAPWATSLYEAR 240  
DB NIAAFGNPKSVTLFGESAGAAVSLSLSPGSHSLFTRAILQSGSPNAPWATSLYEAR 268  
QY 209 NIAAFGNPKSVTLFGESAGAAVSLSLSPGSHSLFTRAILQSGSPNAPWATSLYEAR 268  
DB 209 NIAAFGNPKSVTLFGESAGAAVSLSLSPGSHSLFTRAILQSGSPNAPWATSLYEAR 268  
QY 241 NRTNLAKLTGCGRENTEITIKLRNKPDEIILNEAFVVPYGTPLSVNFGPTVDGFLT 300  
DB NRTNLAKLTGCGRENTEITIKLRNKPDEIILNEAFVVPYGTPLSVNFGPTVDGFLT 328  
QY 269 NRTNLAKLTGCGRENTEITIKLRNKPDEIILNEAFVVPYGTPLSVNFGPTVDGFLT 328  
DB 269 NRTNLAKLTGCGRENTEITIKLRNKPDEIILNEAFVVPYGTPLSVNFGPTVDGFLT 328  
QY 301 DMPDILLELQGFKKTKQLLVGNKDEGTPFLVYAGPGSKNNSIITRKEFOEGSKITFPFG 360  
DB DMPDILLELQGFKKTKQLLVGNKDEGTPFLVYAGPGSKNNSIITRKEFOEGSKITFPFG 360

Db 329 DMPDILLELGQFKKTQILVGNKDEGTAFVYGA PGSKDNNSITTRKEFGELKIFPPG 388  
Qy 361 VSEFGKESILFHYTDWDQRPENYREALGDVGVDFNFCALPFTKFSKSEGNNAFFYY 420  
Db 389 VSEFGKESILFHYTDWDQRPENYREALGDVGVDFNFCALPFTKFSKSEGNNAFFYY 448  
Qy 421 FEHRSSKLPMPENMGVHGVEIEFVFGPLERRDNYTKAEIISRSIVKRWANPAKYGNP 480  
Db 449 FEHRSSKLPMPENMGVHGVEIEFVFGPLERRDNYTKAEIISRSIVKRWANPAKYGNP 508  
Qy 481 NETQNNSTSWPVFKSTEQKYLTLNTBSTRIMTKLRAQOCRFWTSFPFKVLEMTGNIDAE 540  
Db 509 NETQNNSTSWPVFKSTEQKYLTLNTBSTRIMTKLRAQOCRFWTSFPFKVLEMTGNIDAE 568  
Qy 541 MEWKAGFHRNNNTMMDKQNFNDYTSKESCVGL 574  
Db 569 MEWKAGFHRNNNTMMDKQNFNDYTSKESCVGL 602

## RESULT 23

ID ADR01045 standard; protein; 574 AA.  
AC ADR01045;  
XX

DT 23-SEP-2004 (first entry)  
XX

DE Butyrylcholinesterase A328W/S287G/F227A/A199S variant.  
XX

KM butyrylcholinesterase; cocaine-induced condition;  
KW cocaine-based butyrylcholinesterase substrate; cocaine-overdose;  
KW cocaine addiction; human; butyrylcholinesterase variant.  
XX

OS Homo sapiens.  
XX

OS Synthetic.  
XX

PN US2004121970-A1.  
XX

PD 24-JUN-2004.  
XX

PF 20-DEC-2002; 2002US-00324466.  
XX

PR 20-DEC-2002; 2002US-00324466.  
XX

PA (WATK/) WATKINS J D.  
XX (PANC/) PANCOCK J D.

PI Watkins JD, Pancook JD;  
XX

DR WPI; 2004-468195/44.  
XX N-PSDB; ADR01044.

PT New butyrylcholinesterase variant polypeptide, useful in treating cocaine  
XX -induced condition, i.e. cocaine-overdose or cocaine addiction.

PS Claim 1; SEQ ID NO 12; 131p; English.  
XX

CC The invention describes a butyrylcholinesterase variant polypeptide (I)  
CC comprising any of the 21 sequences of 57 amino acids each (EVEN SEQ ID  
CC NOS: 2-42) or their functional fragments. Also described are: a nucleic  
CC acid encoding (I) comprising any of the 21 nucleic acid sequences of 2416  
CC bp each (ODD SEQ ID NOS: 1-41) or their fragments; a method of treating a  
CC cocaine-induced condition; and a method of hydrolysing a cocaine-based  
CC butyrylcholinesterase substrate. (I) is butyrylcholinesterase variant  
CC polypeptide comprising any of the 21 sequences of 57 amino acids each  
CC (EVEN SEQ ID NOS: 2-42), encoded by a nucleic acid comprising any of the  
CC 21 nucleic acid sequences of 2416 bp each (ODD SEQ ID NOS: 1-41). The  
CC butyrylcholinesterase variant polypeptides and nucleic acids and methods  
CC are useful in treating cocaine-induced condition i.e. cocaine-overdose or  
CC cocaine addiction. This is the amino acid sequence of a human  
CC butyrylcholinesterase variant.  
XX

XX Sequence 574 AA;  
XX

Query Match 99.5%; Score 3095; DB 8; Length 574;  
Best Local Similarity 99.5%; Pred. No. 5,4e-277;  
Matches 571; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EDDIIITKNGKRGKNNLTVFGGTVTAFLGIPYAPPLGRLRKPKPSLTKWSINWATK 60  
Db 1 EDDIIITKNGKRGKNNLTVFGGTVTAFLGIPYAPPLGRLRKPKPSLTKWSINWATK 60  
Qy 61 YANSCCNIDQSPFGFGSEMMNPNTDLSBDCLYANWIPAPKXATVLIWYGGGQF 120  
Db 61 YANSCCNIDQSPFGFGSEMMNPNTDLSBDCLYANWIPAPKXATVLIWYGGGQF 120  
Qy 121 GTSSLHYDQKFLARVERVIVSMNYRVGALGFALPGNEADGNNMGLPQOLALQWVK 180  
Db 121 GTSSLHYDQKFLARVERVIVSMNYRVGALGFALPGNEADGNNMGLPQOLALQWVK 180  
Qy 181 NIAAFGNPKSVTLFGSSAGAASVSLHLSPGSHSLFTRAILQSGSFNAPWATVSLYEAR 240  
Db 181 NIAAFGNPKSVTLFGSSAGAASVSLHLSPGSHSLFTRAILQSGSFNAPWATVSLYEAR 240  
Qy 241 NRTLNLAKLTGCSRENETELIKCLRNKDPQELINLEAFVVPYGTPLGVNFGPTVDGFLT 300  
Db 241 NRTLNLAKLTGCSRENETELIKCLRNKDPQELINLEAFVVPYGTPLGVNFGPTVDGFLT 300  
Qy 301 DMPDILLELGQFKKTQILVGNKDEGTAFVYGA PGSKDNNSITTRKEFGELKIFPPG 360  
Db 301 DMPDILLELGQFKKTQILVGNKDEGTAFVYGA PGSKDNNSITTRKEFGELKIFPPG 360  
Qy 361 VSEFGKESILFHYTDWDQRPENYREALGDVGVDFNFCALPFTKFSKSEGNNAFFYY 420  
Db 361 VSEFGKESILFHYTDWDQRPENYREALGDVGVDFNFCALPFTKFSKSEGNNAFFYY 420  
Qy 421 FEHRSSKLPMPENMGVHGVEIEFVFGPLERRDNYTKAEIISRSIVKRWANPAKYGNP 480  
Db 421 FEHRSSKLPMPENMGVHGVEIEFVFGPLERRDNYTKAEIISRSIVKRWANPAKYGNP 480  
Qy 481 NETQNNSTSWPVFKSTEQKYLTLNTBSTRIMTKLRAQOCRFWTSFPFKVLEMTGNIDAE 540  
Db 481 NETQNNSTSWPVFKSTEQKYLTLNTBSTRIMTKLRAQOCRFWTSFPFKVLEMTGNIDAE 540  
Qy 541 MEWKAGFHRNNNTMMDKQNFNDYTSKESCVGL 574  
Db 541 MEWKAGFHRNNNTMMDKQNFNDYTSKESCVGL 574

## RESULT 24

ID ADR01059 standard; protein; 574 AA.  
AC ADR01059;  
XX

DT 23-SEP-2004 (first entry)  
XX

DE Human butyrylcholinesterase V331L variant.  
XX

KM butyrylcholinesterase; cocaine-induced condition;  
KW cocaine-based butyrylcholinesterase substrate; cocaine-overdose;  
KW cocaine addiction; human; butyrylcholinesterase variant.  
XX

OS Homo sapiens.  
XX

OS Synthetic.  
XX

PN US2004121970-A1.  
XX

PD 24-JUN-2004.  
XX

PF 20-DEC-2002; 2002US-00324466.  
XX

PR 20-DEC-2002; 2002US-00324466.  
XX

PA (WATK/) WATKINS J D.  
XX (PANC/) PANCOCK J D.

XX Watkins JD, Pancook JD;  
PI  
XX WPI, 2004-468195/44.  
DR N-PSDB; ADR01058.  
XX

PT New butyrylcholinesterase variant polypeptide, useful in treating cocaine  
PT -induced condition, i.e. cocaine-overdose or cocaine addiction.  
XX  
XX Claim 1; SEQ ID NO 26; 131pp; English.

XX The invention describes a butyrylcholinesterase variant polypeptide (I)  
CC comprising any of the 21 sequences of 57 amino acids each (EVEN SEQ ID  
CC NOS: 2-42) or their functional fragments. Also described are: a nucleic  
CC acid encoding (I) comprising any of the 21 nucleic acid sequences of 2416  
CC bp each (ODD SEQ ID NOS: 1-41) or their fragments; a method of treating a  
CC cocaine-induced condition; and a method of hydrolysing a cocaine-based  
CC butyrylcholinesterase substrate. (I) is butyrylcholinesterase variant  
CC polypeptide comprising any of the 21 sequences of 57 amino acids each  
CC (EVEN SEQ ID NOS: 2-42), encoded by a nucleic acid comprising any of the  
CC 21 nucleic acid sequences of 2416 bp each (ODD SEQ ID NOS: 1-41). The  
CC butyrylcholinesterase variant polypeptides and nucleic acids and methods  
CC are useful in treating cocaine-induced condition i.e. cocaine-overdose or  
CC cocaine addiction. This is the amino acid sequence of a human  
CC butyrylcholinesterase variant.  
XX

XX Sequence 574 AA:

Query Match 99.5%; Score 3093; DB 8; Length 574;  
Best Local Similarity 99.7%; Pred. No. 8.3e-277;  
Matches 572; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDDIIATKKGKRGKGNLTVFGGTVTAFLGIPYAPPLGRLPKKPSLTGKSDINWATK 60  
DB 1 EDDIIATKKGKRGKGNLTVFGGTVTAFLGIPYAPPLGRLPKKPSLTGKSDINWATK 60  
QY 61 YANSCCNIDQSPFGHSEMNPNNTDLSBDCLYLNWVTPAPKKNATVLIWYGGGFQT 120  
DB 61 YANSCCNIDQSPFGHSEMNPNNTDLSBDCLYLNWVTPAPKKNATVLIWYGGGFQT 120  
QY 121 GTSSLHYDQKFLARVERVIVSMNRYVGAAGLALGNPAPKNGMLFPOQLALQWVK 180  
DB 121 GTSSLHYDQKFLARVERVIVSMNRYVGAAGLALGNPAPKNGMLFPOQLALQWVK 180  
QY 181 NIAAFGNPKSVTLFGESAGAASVSLHLSPGSHLFTFRAIIQSGSFNAPWATSYEAR 240  
DB 181 NIAAFGNPKSVTLFGESAGAASVSLHLSPGSHLFTFRAIIQSGSFNAPWATSYEAR 240  
QY 241 NRTLNLAKTGCSRENETEIKCLRNKDPQRIILNEAFVVPYGTPLSVNFGPTVDSFLT 300  
DB 241 NRTLNLAKTGCSRENETEIKCLRNKDPQRIILNEAFVVPYGTPLSVNFGPTVDSFLT 300  
QY 301 DMPDILLLEQPKTKTQIILVGNKDEGTMFLVYGA PGSKNNSTITRKEPQGLKIFPPG 360  
DB 301 DMPDILLLEQPKTKTQIILVGNKDEGTMFLVYGA PGSKNNSTITRKEPQGLKIFPPG 360  
QY 361 VSEFGKESILFHYTDWDDORPENYREALGDVGDYNYFCALFETKFSWGNNAFFYY 420  
DB 361 VSEFGKESILFHYTDWDDORPENYREALGDVGDYNYFCALFETKFSWGNNAFFYY 420  
QY 421 FEHSSSKLPWPEWNGVNHGYEIEFVFGPLERRRDYTAEBIISRSIVKMANPAKYGNP 480  
DB 421 FEHSSSKLPWPEWNGVNHGYEIEFVFGPLERRRDYTAEBIISRSIVKMANPAKYGNP 480  
QY 481 NETQNNSTSWPEVSTKQKYLTLNTESTRIMTKLAQOCCRFWTSFPFVLEMTGNIDAE 540  
DB 481 NETQNNSTSWPEVSTKQKYLTLNTESTRIMTKLAQOCCRFWTSFPFVLEMTGNIDAE 540  
QY 541 MEMKAGFHRNNMYMDKQNFNDYTSKESCYGL 574  
DB 541 MEMKAGFHRNNMYMDKQNFNDYTSKESCYGL 574

RESULT 25

ADRO1075  
ID ADR01075 standard; protein; 574 AA.

AC ADR01075;

DT 23-SEP-2004 (first entry)

DE Human butyrylcholinesterase A199S variant.

XX butyrylcholinesterase; cocaine-induced condition;

KW cocaine-based butyrylcholinesterase substrate; cocaine-overdose;

KM cocaine addiction; human; butyrylcholinesterase variant.

OS Homo sapiens.

OS Synthetic.

PN US2004121970-A1.

PD 24-JUN-2004.

PF 20-DEC-2002; 2002US-00324466.

PR 20-DEC-2002; 2002US-00324466.

PA (WATK/) WATKINS J D.

PA (PANC/) PANCOCK J D.

PI Watkins JD, Pancook JD;

XX WPI, 2004-468195/44.

DR N-PSDB; ADR01074.

PT New butyrylcholinesterase variant polypeptide, useful in treating cocaine

PT -induced condition, i.e. cocaine-overdose or cocaine addiction.

XX Claim 1; SEQ ID NO 42; 131pp; English.

XX The invention describes a butyrylcholinesterase variant polypeptide (I)  
CC comprising any of the 21 sequences of 57 amino acids each (EVEN SEQ ID  
CC NOS: 2-42) or their functional fragments. Also described are: a nucleic  
CC acid encoding (I) comprising any of the 21 nucleic acid sequences of 2416  
CC bp each (ODD SEQ ID NOS: 1-41) or their fragments; a method of treating a  
CC cocaine-induced condition; and a method of hydrolysing a cocaine-based  
CC butyrylcholinesterase substrate. (I) is butyrylcholinesterase variant  
CC polypeptide comprising any of the 21 sequences of 57 amino acids each  
CC (EVEN SEQ ID NOS: 2-42), encoded by a nucleic acid comprising any of the  
CC 21 nucleic acid sequences of 2416 bp each (ODD SEQ ID NOS: 1-41). The  
CC butyrylcholinesterase variant polypeptides and nucleic acids and methods  
CC are useful in treating cocaine-induced condition i.e. cocaine-overdose or  
CC cocaine addiction. This is the amino acid sequence of a human  
CC butyrylcholinesterase variant.  
XX

XX Sequence 574 AA:

Query Match 99.5%; Score 3093; DB 8; Length 574;  
Best Local Similarity 99.7%; Pred. No. 8.3e-277;  
Matches 572; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDDIIATKKGKRGKGNLTVFGGTVTAFLGIPYAPPLGRLPKKPSLTGKSDINWATK 60  
DB 1 EDDIIATKKGKRGKGNLTVFGGTVTAFLGIPYAPPLGRLPKKPSLTGKSDINWATK 60  
QY 61 YANSCCNIDQSPFGHSEMNPNNTDLSBDCLYLNWVTPAPKKNATVLIWYGGGFQT 120  
DB 61 YANSCCNIDQSPFGHSEMNPNNTDLSBDCLYLNWVTPAPKKNATVLIWYGGGFQT 120  
QY 121 GTSSLHYDQKFLARVERVIVSMNRYVGAAGLALGNPAPKNGMLFPOQLALQWVK 180  
DB 121 GTSSLHYDQKFLARVERVIVSMNRYVGAAGLALGNPAPKNGMLFPOQLALQWVK 180  
QY 181 NIAAFGNPKSVTLFGESAGAASVSLHLSPGSHLFTFRAIIQSGSFNAPWATSYEAR 240  
DB 181 NIAAFGNPKSVTLFGESAGAASVSLHLSPGSHLFTFRAIIQSGSFNAPWATSYEAR 240

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Db      181 NIAFGGNPKSVTLFGSSGGAASVSIHLSPGSHSLFTRAIIQSGSFNAPMAVTSIYEAR 240
Qy      241 NRTLNIAKLTCGSRNENETETIICKLRNKDPOEILNBAFVVPYGTPLSVNFGPTVDGDFLT 300
Db      241 NRTLNIAKLTCGSRNENETETIICKLRNKDPOEILNBAFVVPYGTPLSVNFGPTVDGDFLT 300
Qy      301 DMPDILIELGQFKKTQILVGVNDEGTWFLVYGAPGFSKDNNSIITRKEFOEGLKIFPPG 360
Db      301 DMPDILIELGQFKKTQILVGVNDEGTWFLVYGAPGFSKDNNSIITRKEFOEGLKIFPPG 360
Qy      361 VSEFGKESILFHYTDWDDQRPENYRALGDVVDYVNFICPALEFTKKFSKGNNAFFYY 420
Db      361 VSEFGKESILFHYTDWDDQRPENYRALGDVVDYVNFICPALEFTKKFSKGNNAFFYY 420
Qy      421 FEHRSKLPMPWEMGVHGYEIEFVFGPLERDNTYKAEIISRSIVKRWANPAKYGNP 480
Db      421 FEHRSKLPMPWEMGVHGYEIEFVFGPLERDNTYKAEIISRSIVKRWANPAKYGNP 480
Qy      481 NETQNNSTSWPVFKSTEQKTLTLNTESTRIWTKLRAQOCRFWTSFPPKVLMTGNIDEAE 540
Db      481 NETQNNSTSWPVFKSTEQKTLTLNTESTRIWTKLRAQOCRFWTSFPPKVLMTGNIDEAE 540
Qy      541 WEWKAGFHRNNYMMDMKQNDYTSKESCVGL 574
Db      541 WEWKAGFHRNNYMMDMKQNDYTSKESCVGL 574

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Search completed: January 6, 2005, 09:56:17  
 Job time : 164 secs

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